

From: Hamud, Fozia
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Fozia Hamud
Patent Examiner
Remsen 4D64
Mail Box: Remsen 4C70
(571) 272-0884
Art Unit 1647

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Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
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Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 20:14:15 ; Search time 5659 Seconds

(without alignments)
10557.569 Million cell updates/sec

Title: US-09-598-443-1

Perfect score: 1233
1 atgcacagatgctcgtatgtag.....tgccacagatgtagatgtag 1233

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
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2: gb bta: *
3: gb in: *
4: gb om: *
5: gb ov: *
6: gb pac: *
7: gb ph: *
8: gb pl: *
9: gb pr: *
10: gb ro: *
11: gb str: *
12: gb sy: *
13: gb un: *
14: gb vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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3	1233	100.0	1627	9	BC003591
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7	1230.4	99.8	1233	9	CR457338
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ALIGNMENTS

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DEFINITION
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VERSION
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SOURCE
ORGANISM
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COMMENT
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BD103586.1 GI:22649160
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Sims,J.E.
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ACCESSION BC025953
VERSION BC025953.1 GI:19684156
KEYWORDS MGC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 1618)
Strausberg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altehoe, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Ma, S.I., Wang, D., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stepleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheet, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Scheraga, H.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dietterle, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,
Scheraga, H., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1618)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Heiao, Martin Krzywinski, Reta Katsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candace McLeary, Steven
Ness, Pawan Pandob, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalhe, Michael Smith, Lorraine Spence, Jeff Strotz,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

AUTHORS	Strasberg, R. L., Feinold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Sherman, C. M., Altschul, S. F., Zeeberg, B., Buettner, K. H., Schaefer, C. F., Bhattacharya, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., DiGiuseppe, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Schapleton, M., Soares, M. B., Bonaldi, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Udell, T. B., Toshitsugu, S., Carninci, P., Prange, C., Raha, S. S., Loguanello, N. A., Peters, G. J., Abramson, R. D., Mullany, S. J., Bosak, S. A., McEwen, P. J., McKernan, K. D., Malek, U. A., Gunnarsson, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hult, S. W., Villalón, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fehey, J., Helton, E., Kettelman, M., Madan, A. C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Scherchenko, Y., Bouffard, G. C., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Skalka, U., Smalls, D. E., Schmecher, A., Schein, J. E., Jones, S. J., and Marra, M. A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLISHED	12477932
REFERENCE	2 (bases 1 to 1627)
AUTHORS	Strasberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (20-FEB-2001) National Institutes of Health, Mammalian

REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT	Contact: MGC help desk

CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Crow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guit, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Morin, Teika Olson, Diana Palomquist, Anna Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angelique Schermer, Ursula Skalak, Duane Smalau, Jeff Stott, Miranda Tsai, George Yang, Jacques Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLAST at: <http://image.llnl.gov>
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DEFINITION Homo sapiens s1ngle IG-IL-IR-related molecule (SIGIRR).
ACCESSION AK172830
VERSION AK172830.1 GI:47077852
KEYWORDS oligo capping; file (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Matsubara, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H., Oka, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isega, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1657)
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (22-APR-2004) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shitokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: shichan@mail.fms.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5' - 3' end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
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VERSION AK025099.1 GI:10437546
KEYWORDS oligo capping; fig (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Kawabata, A., Hiki, J., Kobatake, N., Inagaki, H., Ikema, Y.,
Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Odayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1695)

REFERENCE
AUTHORS Sugano, S., Suzuki, Y., Ota, T., Odayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
Fax: 81-3-5449-5416)

COMMENT
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
constructing: 5' - & 3' - end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES
source
1.1695

FEATURES
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RNVSRPTPFYCLVSRDM"

Query Match 100.0%; Score 1233; DB 9; Length 1695;
Best Local Similarity 100.0%; Pred. No. 3.1e-182;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAGGTGCTGATGATGAGGCCCCGTGACTTCTCTCCCGCTGAAGACCAAGGCTG 60
DB 227 ATGCCAGGTGCTGATGATGAGGCCCCGTGACTTCTCTCCCGCTGAAGACCAAGGCTG 286
QY 61 AGGCTGACCTTGGGAGCTCAGTGGCTTGAACCTGACCGCTTGGGTAGTCTTGGAGCC 120
DB 287 AGGCTGACCTTGGGAGCTCAGTGGCTTGAACCTGACCGCTTGGGTAGTCTTGGAGCC 346
QY 121 CACTGCTCCCTGCTTCACTGCTCAAGTGGCTGAAGAAGCGGCTTCCATTTGGGAATTGGGG 180
DB 347 CACTGCTCCCTGCTTCACTGCTCAAGTGGCTGAAGAAGCGGCTTCCATTTGGGAATTGGGG 406
QY 181 CACTGAGCTCCAGAGTACTCTGGGCTCAAGGCGCAACCTGTCAGAGGCTTGTGCTC 240
DB 407 CACTGAGCTCCAGAGTACTCTGGGCTCAAGGCGCAACCTGTCAGAGGCTTGTGCTC 466
QY 241 AGTGTCTGGGGAGTCAACGTGACCAAGCACTGAAGTCTATGGGAGCTTCACTGCTCATC 300
DB 467 AGTGTCTGGGGAGTCAACGTGACCAAGCACTGAAGTCTATGGGAGCTTCACTGCTCATC 526
QY 301 CAGAATCATAGCTTCTCTCTTCACTTTCAGAGAGCTGGCCCTTCAAGCCACGTGGCT 360
DB 527 CAGAATCATAGCTTCTCTCTTCACTTTCAGAGAGCTGGCCCTTCAAGCCACGTGGCT 586
QY 361 GGGGCTGGGCGCCCTCTGTCGCTGAGGCGGCTGCTGCTGAGGCGCCCTGCTCATATGTC 420
DB 587 GGGGCTGGGCGCCCTCTGTCGCTGAGGCGGCTGCTGCTGAGGCGCCCTGCTCATATGTC 646
QY 421 AAGTGCCTCTCAAGCTGCTGCTGATCAAGAGCGCTATGGGAGTGAATTAAC 480
DB 647 AAGTGCCTCTCAAGCTGCTGCTGATCAAGAGCGCTATGGGAGTGAATTAAC 706
QY 481 GACGGAGACTCTACAGACCTTACGCTCTTACAGAGATGCCCCGAGACCGCAAGTTC 540
DB 707 GACGGAGACTCTACAGACCTTACGCTCTTACAGAGATGCCCCGAGACCGCAAGTTC 766
QY 541 GTGAATTCATCTTAAGCGGAGCTGAGCGGCGCTGAGGAGCTTCAAGCTCTTCTGAGC 600
DB 767 GTGAATTCATCTTAAGCGGAGCTGAGCGGCGCTGAGGAGCTTCTTCTCTGAGC 826
QY 601 GACCGGACCTCTGCGCGGCTGAGGAGCTTCTGCGGACCTTGTGTAACCTGAGCCGC 660
DB 827 GACCGGACCTCTGCGCGGCTGAGGAGCTTCTGCGGACCTTGTGTAACCTGAGCCGC 886
QY 661 TGCCGACGCTCATGCTGCTTTCGAGAGCGCTTCTGAGCGGCGCTGAGGAGCTGAGCCAC 720
DB 887 TGCCGACGCTCATGCTGCTTTCGAGAGCGCTTCTGAGCGGCGCTGAGGAGCTGAGCCAC 946
QY 721 AGCTTCGGGAGAGGCTGAGCGGCTGAGAGCTTCAAGCGGAGACCACTTCATCAC 780
DB 947 AGCTTCGGGAGAGGCTGAGCGGCTGAGAGCTTCAAGCGGAGACCACTTCATCAC 1006
QY 781 TTGAGAGGCGAGAGGCGGACCCCGGACCCGCGCTTCCGCTGCTGCGGACGACCCG 840
DB 1007 TTGAGAGGCGAGAGGCGGACCCCGGACCCGCGCTTCCGCTGCTGCGGACGACCCG 1066
QY 841 CACTGCTGACCTTGTCTCTGAGAGCGGCGCTTCCGCTGCTTCTTCCGATTTTGG 900
DB 1067 CACTGCTGACCTTGTCTCTGAGAGCGGCGCTTCCGCTGCTTCTTCCGATTTTGG 1126

QY 901 AAAGAAGTGCAGCTGGGCTGGCCCGGGAAGGTGGGCTACAGGCCGGTGGAGAGACCC 960
DB 1127 AAAAGAGTGCAGCTGGGCTGGCCCGGGAAGGTGGGCTACAGGCCGGTGGAGAGACCC 1186
QY 961 CAGACGAGCTGCAG 1020
DB 1187 CAGACGAGCTGCAG 1246
QY 1021 GGGCGGGGCTGGAGCTCAGAGGTGAGCCCGAGCCCTGAGGGGAGAGAGAGAGAGAGAG 1080
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QY 1141 CCGAGCAGCAG 1200
DB 1367 CCGAGCAGCAG 1426
QY 1201 TTCTACTGCTGCTGCTGCTCAAGAGATGATATGTAG 1233
DB 1427 TTCTACTGCTGCTGCTGCTCAAGAGATGATATGTAG 1459

RESULT 6
AX058610
LOCUS AX058610 1659 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 17 from Patent WO0075321.
ACCESSION AX058610
VERSION AX058610.1 GI:12310952
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Shimkete, R.A., Fernandes, E., Herrman, J. and Vernet, C.
TITLE Polynucleotides and membrane-bound polypeptides encoded thereby
JOURNAL Patent: WO 0075321-A 17 14-DEC-2000;
Curagen Corporation (US)
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ORIGIN
Query Match 99.9%; Score 1231.4; DB 6; Length 1659;
Best Local Similarity 99.9%; Pred. No. 5.6e-182;
Matches 1232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCAGGTGCTGTGATAGAGCCCTGACCTTCCTCCCGCTGAGACAGAGCTG 60
DB 244 ATGCCAGGTGCTGTGATAGAGCCCTGACCTTCCTCCCGCTGAGACAGAGCTG 303
QY 61 AGGCTGCTTGGGAGAGCTCAGTGGCTCTGAACAGAGCTTGGAGTCTTGGAGCC 120
DB 304 AGGCTGCTTGGGAGAGCTCAGTGGCTCTGAACAGAGCTTGGAGTCTTGGAGCC 363

QY 121 CACTGCTCCCTGCTTCACTGCTCACTGCTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 364 CACTGCTCCCTGCTTCACTGCTCACTGCTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 423
QY 181 CACTAGAGCTCCAGAGAGTACTCTGGGTGAAAGGCAACCTGTGAGAGAGTCTGTGTCC 240
DB 424 CACTAGAGCTCCAGAGAGTACTCTGGGTGAAAGGCAACCTGTGAGAGAGTCTGTGTCC 483
QY 241 AGTGTCTGGAGAGTCAAGTGAACGAGACCTGAAGTCTATGGAGCTTCACTGTCTCATC 300
DB 484 AGTGTCTGGAGAGTCAAGTGAACGAGACCTGAAGTCTATGGAGCTTCACTGTCTCATC 543
QY 301 CAGAACTCAGCTTCTCTCTCTTCACTCTTCAAGAGAGTGGCTTCAAGAGAGAGTGGCT 360
DB 544 CAGAACTCAGCTTCTCTCTCTTCACTCTTCAAGAGAGTGGCTTCAAGAGAGAGTGGCT 603
QY 361 GCGGTGCTGGAGCTCCCTCTGAGTCTGAGTGGAGCCCTGAGTGGAGCCCTGAGTGGAGT 420
DB 604 GCGGTGCTGGAGCTCCCTCTGAGTCTGAGTGGAGCCCTGAGTGGAGCCCTGAGTGGAGT 663
QY 421 AAGTGCCTGCTCAAGTGTGCTCTGTGTAACAGAGACGAGATGGAGAGTGGAGATTAAC 480
DB 664 AAGTGCCTGCTCAAGTGTGCTCTGTGTAACAGAGACGAGATGGAGAGTGGAGATTAAC 723
QY 481 GACGGAGAGCTTACAGAGCTTACGCTTCTCTTCAAGAGAGTGGCTTCAAGAGAGAGTGG 540
DB 724 GACGGAGAGCTTACAGAGCTTACGCTTCTCTTCAAGAGAGTGGCTTCAAGAGAGAGTGG 783
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DB 844 GACGGAGAGCTTCTGAGCGAGCTGAGAGCTTCCGAGAGCTTGTGTAACCTTGGAGAGCGC 903
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DB 964 AGCTTCCGAGAGAGAGCTGAGCGAGCTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAG 1023
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DB 1024 TTGAG 1083
QY 841 CACTGTGAGCTTGTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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QY 901 AAAGAAGTGAAGCTGGAG 960
DB 1144 AAAGAAGTGAAGCTGGAG 1203
QY 961 CAGACGAGCTGCAG 1020
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DB 1264 GGGCGGGGCTGGAGCTTCAAGAGTGGAGCCCGAGCCCTGAGGGGAGAGAGAGAGAGAG 1323
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QY 1141 CCGAGCAGCAG 1200
DB 1384 CCGAGCAGCAG 1443

QY 1201 TTCTACTGCTGGTGTCTCAAGATGATATAG 1233
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Db 1444 TTCTACTGCTGGTGTCTCAAGATGATATAG 1476

RESULT 7
CR457338
LOCUS 1233 bp mRNA 1linear PRI 03-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834H0613D for gene SIGIRR, single Ig IL-1R-related molecule; complete cds, incl. stopcodon.
ACCESSION CR457338
VERSION CR457338.1 GI:48146792
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1233)
AUTHORS Ebert,L., Schlick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1233)
AUTHORS Ebert,L., Schlick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE Direct Submision
JOURNAL Submitted (03-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
COMMENT RZPD; RZPD0834H0613D, ORFNO 2417
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834H0613D RZPDLIB;
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www.rzpd.de/cgi-bin/products/showlib.pl.cgi?response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Airlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full length expression clones generated by RZPD.
This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. AAAAAA GCA GGC (ATG).
The last base of the last coding triplet has been changed to T, which might lead to an amino acid change at the C terminus of the polypeptide.
The stop codon has been set to TAA followed by TTAACCGCTTCTT. att. Compared to the reference sequence NM_021805 we found amino acid exchange(s) at position (first base of changed triplet): 1228(met->ile)
Clone distribution: http://www.rzpd.de/products/orfclones/.
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ORIGIN

Query Match 99.8%; Score 1230.4; DB 9; Length 1233;
Best Local Similarity 99.9%; Pred. No. 8.6e-182;
Matches 1231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCAGGTCGTGATAGTGGGCCCCGTGCTTCCTCTCCCGCTGAAGCCAGGTCG 60
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Db 1 ATGCCAGGTCGTGATAGTGGGCCCCGTGCTTCCTCTCCCGCTGAAGCCAGGTCG 60

QY 61 AGGCTGCTGGGGCAGCTCAATGAGCTTGAACCTGACCGGCTTGGAGTCTTGGAGCC 120
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QY 121 CACTGCTCCCTGCTTCACTGCTGCTGAAGAAGCGGCTTCAATTGGGAATTGGGGCC 180
|||||
Db 121 CACTGCTCCCTGCTTCACTGCTGCTGAAGAAGCGGCTTCAATTGGGAATTGGGGCC 180

QY 181 CACTACAGCTCCAGAGTACTCTGGGTCAGAGGCCAACCTGTCAGAGGTCCTGTGTC 240
|||||
Db 181 CACTACAGCTCCAGAGTACTCTGGGTCAGAGGCCAACCTGTCAGAGGTCCTGTGTC 240

QY 241 AGTGTCTGGGGGTCAACGCTGACAGCACTGAAGTATGGGGCTTCACTGCTCATC 300
|||||
Db 241 AGTGTCTGGGGGTCAACGCTGACAGCACTGAAGTATGGGGCTTCACTGCTCATC 300

QY 301 CAGACATCAGCTTCTCTCTTCACTTTCAGAGAGCTGGCCCTTCAAGCCAGTGGCT 360
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Db 301 CAGACATCAGCTTCTCTCTTCACTTTCAGAGAGCTGGCCCTTCAAGCCAGTGGCT 360

QY 361 GGGGTCGAGGCTCCCTCGGTCGCTGGGCTGAGGCTGAGGCTGAGTATGTC 420
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Db 361 GGGGTCGAGGCTCCCTCGGTCGCTGGGCTGAGGCTGAGGCTGAGTATGTC 420

QY 421 AAGTCCGCTCAACGCTGCTCTTGTGTAACAAGAGCGCTATGGAGGTGAGATTAAC 480
|||||
Db 421 AAGTCCGCTCAACGCTGCTCTTGTGTAACAAGAGCGCTATGGAGGTGAGATTAAC 480

QY 481 GACGGGAAGCTTACGAGCGCTTACGCTCTTACAGAGACTGCCCCGAGGACCGCAAGTTC 540
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QY 541 GTGAATTCATCTTAAGCGCAGCTGAGCGGCGTGGGGGCTTCAAGCTCTTCGTGAC 600
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QY 601 GACCGGAGCTCTGCGCGCGGCTGAGCGGCTTCCGCGGAGCTTGTGTAACCTGAGCGCG 660
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Db 601 GACCGGAGCTCTGCGCGCGGCTGAGCGGCTTCCGCGGAGCTTGTGTAACCTGAGCGCG 660

QY 661 TGGCGAGCGCTCATGCTGCTTTTGAACGCTTCTCTGAGCGGCGCTGTGTGACGAC 720
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Db 661 TGGCGAGCGCTCATGCTGCTTTTGAACGCTTCTCTGAGCGGCGCTGTGTGACGAC 720

QY 721 AGCTTCGGGAGGAGGCTGTGCGGCTGTGAGAGCTACCGCGAGACCATCTTCATCAC 780
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QY 781 TTGAGAGGCGAAGAGGCGACCCCGGCAACCCGCGCTCGCTGTGCGCGACACCGC 840
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Db 781 TTGAGAGGCGAAGAGGCGACCCCGGCAACCCGCGCTCGCTGTGCGCGACACCGC 840

QY 841 CACTGTGTACCTTGTGCTGTGAGAGCGCGGCTCGGTGACTCTTCTCCGATTTTGG 900
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Db 841 CACTGTGTACCTTGTGCTGTGAGAGCGCGGCTCGGTGACTCTTCTCCGATTTTGG 900

Db 1257 CACGGCAGTGAATGATGTCTCTGACCTCGGCTCTGAAACTACAGTGCAGCAGAC 1316
QY 1201 TTCTACTGCTGCTGCTCAAGATGATATGTAG 1233
Db 1317 TTCTACTGCTGCTGCTGATGATGTGTAG 1349

RESULT 11
AF239957 1421 bp mRNA linear ROD 21-MAR-2000
LOCUS AF239957
DEFINITION Mus musculus single Ig II-IR-related protein mRNA, complete cds.
ACCESSION AF239957.1 GI:7271942
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE 1 (bases 1 to 1421)
AUTHORS Poltorak, A. and Beutler, B.
TITLE Molecular cloning of mouse SIGIRR, an orphan receptor with a
Toll-like cytoplasmic domain
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1421)
AUTHORS Poltorak, A. and Beutler, B.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2000) Internal Medicine, UT Southwestern Medical
Center/HMT, 5323 Harry Hines Boulevard, Dallas, TX 75235-9050, USA
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ORIGIN
Query Match 69.5%; Score 856.6; DB 10; Length 1421;
Best Local Similarity 81.5%; Pred. No. 1,1e-123;
Matches 1004; Conservative 0; Mismatches 225; Indels 3; Gaps 1;
QY 1 ATGCCAGGTCGTGTAGTGGCCCTGACCTCTCCCGCTGGAAGCAGGTCGTG 60
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QY 61 AGGCTGCTCTTGGGCAAGCTCAGTGGCTCTGAAGTGCAGGCTTGGGTAGTCTGAGGCC 120
Db 169 GGTCTTGCCCTTGGCAGAGAGATTGCTTGAATTGACAGACTTGGGTCTCTAGGCC 228
QY 121 CACTGCTCCTGCTTCACTCAGTGCAGTGGCTGAAGAAGCGGCTTCCATTGGGAATTGGGGCC 180
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QY 181 CACTACAGCTCAAGAGTACTCTCTGGGTCAAGGCCAAGCTGTCAGAGGTGCTGTGTCC 240
Db 289 CACTTACGCTTCAATGAGACTTCTGGGTCAAGGCCCAACTTCTCAGA---GATTGTGTC 345
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Db 346 AGTGTCTGTGTCTCAACTTGAACCAATGCAGAGACTATGAACTTCACTGTCTGTG 405
QY 301 CAGAACATAGCTTCTCTCTTCACTCTTCAAGAGAGCTGGCCCTTCAAGCCAGTGGCT 360
Db 406 TGGAAATGATAGCTCCCATTCCTTCACTCTTGGCGAGCTGGCCCTCTGGCCATGTGGCT 465
QY 361 GCGGTGCTGGCTCCCTCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 466 GCAGTACTGGCTTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
QY 421 AAGTCCGTCTCAAGCTGTGCTCTGTGTAACAAGACGCGTATGGGAGAGTGAATTAAC 480
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Db 1126 GGGCGGGGAGTGAAGTCAAGCTGATTCAGAGACCTGAGGGAGACCTGGGTGTCGGGGA 1185
QY 1081 CTTGTTTTGAGAGGCTCACTAGCTTCAAGCAGACCAAGTGTGGGTCTGCTGGAGAGAGC 1140
Db 1186 CTGTCTTTGGGAGGAGCAGCACTCACTGAGAGAGAGAGAGATGAGAGAGAGC 1245
QY 1141 CGAGAGCAGGAAGTGAAGCTTCTGATCTTGGGCTGCGAAACTCAAGTGTCCGACAGAC 1200
Db 1246 CACGGCAGTGAATGTATGTCTGTGACTCTGAGCTCTGNAACTCAAGTGCAGGACAGAC 1305
QY 1201 TTCTACTGCTGCTGCTCAAGATGATGTATGTA 1232
Db 1306 TTCTACTGCTGCTGCTGATGATGTATGTA 1337

RESULT 12
AF113795 1540 bp mRNA linear ROD 10-MAR-2004
LOCUS AF113795
DEFINITION Mus musculus toll/interleukin-1 receptor 8 (TIR8) mRNA, complete
cds.
ACCESSION AF113795

VERSION	KEYWORDS
SOURCE	ORGANISM
AP113795.1	GI:6714887
REFERENCE	Mus musculus (house mouse)
AUTHORS	Mus musculus Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1540) Garlanda, C., Riva, F., Polentarutti, N., Buracchi, C., Sironi, M., De Bortoli, M., Muzio, M., Bergocchini, R., Scanziani, E., Vecchi, A., Hirsch, E. and Mantovani, A. Intestinal inflammation in mice deficient in Tlr8, an inhibitory member of the Il-1 receptor family Proc. Natl. Acad. Sci. U.S.A. 101 (10), 3522-3526 (2004) 14993616 2 (bases 1 to 1540) Pentoni-Rol, G., Polentarutti, N., Muzio, M. and Mantovani, A. TLR8: a novel toll/interleukin-1 receptor family member Unpublished 3 (bases 1 to 1540) Pentoni-Rol, G., Polentarutti, N., Muzio, M. and Mantovani, A. Direct Submission Submitted (14-DEC-1998) Immunology, Mario Negri Institute, Via Elitrea 62, Milano, MI I-20152, Italy Location/Qualifiers 1. 1540
FEATURES	source

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1. _1540
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115. .j344
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family; cytoplasmic domain similar to other IL-1r family
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RCRLIYVLSDAFLSRPWCOSFRFEDCAIYSPADLSSSLPRKRGVSPDLLSGSCR
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ORIGIN

Query Match	67.0%	Score 826	DB 10	Length 1540
Best Local Similarity	81.0%	Pred. No. 6.1e-119		
Matches 999	Conservative	0	Mismatches 230	Indels 5
				Gaps 3

Qy	ATGCAAGGTGCTGTGAATAGGGCCCCCTBACATTCCTCTCCCGCTGAAAGACACAGGTGCTG	60
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Qy	AGGCCTGCTTTGGGCAGCTCAGTGGCTCTGAACTGCAAGGCTTGGGTAGTCTCTGGGCC	120
Db	GCTCTTGCCCTTGGGACGAGAAGTTGCTTTGAATTGACAGCTTGGGTCTTCTTAGGCC	175
Qy	CACGTCTCTCTGCTTCACTGCTCAGTGGCTGAAAGACGGGCTTCCATTGGGAAATTGGGGGC	180
Db	CAGGTCTCCCAAGCATCTGATCGAGGCTGAAAGATGGTCTGGGCAATTGGGCAATTGGAAAGC	235
Qy	CACGTCTCTCTGCTTCACTGCTCAGTGGCTGAAAGACGGGCTTCCATTGGGAAATTGGGGGC	240
Db	CACGTCTCCCAAGCATCTGATCGAGGCTGAAAGATGGTCTGGGCAATTGGGCAATTGGAAAGC	295
Qy	CACGTCTCTCTGCTTCACTGCTCAGTGGCTGAAAGACGGGCTTCCATTGGGAAATTGGGGGC	300
Db	CACGTCTCCCAAGCATCTGATCGAGGCTGAAAGATGGTCTGGGCAATTGGGCAATTGGAAAGC	351
Qy	AGTGTCTCTGGGGGTCAACGTACACGACTGAAAGTTATGGGGCTTCACTGCTCTCATC	352
Db	AGTGTCTCTGGGGGTCAACGTACACGACTGAAAGTTATGGGGCTTCACTGCTCTCATC	411

QY	301	CAGAACATCAGCTTCTCTCTCTTCACTTTACAGAGAGCTGGCCCTTACAAGCCAGTGGCT	360
Db	412	TGGAAATGCACACTCCCATTTCTTCACTTTTGGGAGAGCCGGCCCTGCTGGGCAATGTGGCT	471
QY	361	GCGGAGCTGGGCTCCCTCTCTGTGTCTGTGTGGCCGCTGCGTGGGCGGCTCTCTATATGC	420
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QY	421	AAGTGCGCTCAACGTGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	480
Db	532	AAAGTGTGGCTGAACATCTCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	591
QY	481	GACGGGAAGCTCTACAGAGCCTTACGTCTCTTACAGCGTCTGCCCGGAGACCGCAATTC	540
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QY	541	GTTAACTTCATCCATAAGCCGAGCTGTGAGGAGGAGGTGGGGGCTTCAAGCTCTTCTGTGAC	600
Db	652	GTTAAATTTTATTTCTGAAAGCTTCAAGTTGAGGAGGAGGTGGGGATACAAATCTTTCTTAGAG	711
QY	601	GACCGCGACCTCTGCGCGCGCTGAGGCTCTCCGCGGACCTCTTGTGTAACTTGAGCGCG	660
Db	712	GACCGCGACCTCTTGGCTCTGGCGGAGGCGCTCTGGCGACCTTTTGTGTAACTTGATGTGC	771
QY	661	TGCGGAGCGCTCATGTGTGTGTCTTTCCGAGCGCTCTTCTGAGCGGGGCTGTGTGACCCAC	720
Db	772	TGTGGGCGCTCATGTGTGTGTCTTTCCAGATCTCTTCTTAAACCGGCGCTGTGTGTAGCCAG	831
QY	721	AGCTTCCGGGAGGGGCTGTGCGGGGTGTGTGAGGTCACCGGACAGCCCATCTTATCAACG	780
Db	832	AGCTTCCGGAG--GGACTGTGCGGCTTACTGTGAGGCTCACCGGACAGCTATCTTCAATCAC	890
QY	781	TTCCGAGGCGCAGAGGCGGACCCCGCGGACCCGCGCTCTGCGCTTGTG--CGCCAGACCG	839
Db	891	TTTGGAGGCGCAGAGGCGGAGGCCATACACCTGTGTCTCGGCTCTGCGCGCACGACCG	950
QY	840	CCACTGTGTACCTTTGCTGCTCTGTGAGGCGCGGCTCGTGTACTCTTCTCCGATTTTTG	899
Db	951	CCACTCTGTGACCTGTGTGCTTTTGGAAAGCTGTGGCTCGGTGACTCTCTTCTCTGTGATTTT	1010
QY	900	GAAAGAAGTGAGCTGGGCGGCTGCGCGGGAAGTGTGCGGTACAGGCGGAGGGAAGAGACC	959
Db	1011	GAAAGAGCTTACGCTAGCATGTGCCACGGAAGTGTGATACAGGCGGAGTGTGAGGAGACCC	1070
QY	960	CCAGACGACGTGAGGACGACGACAAAGGACCCCATCTGTATTTCTTGAGGCGCAGTCCCTGA	1019
Db	1071	TCAAAACCGAATTCAGAGTACAAAGATCCCATCTGTATCTGTAGAGGACGTGTCGCCCA	1130
QY	1020	GCGGCGGGGCTCGGACCTACAGAGTGTGACCCGACCCCTGAGGGGCACTGGGTGTCTCGGG	1079
Db	1131	GCGGCGGGGCTGTGAGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1180
QY	1080	GCCGTGTTTTTGTGAGAGCGATCAGTGTCCACCGCACACAGATGGGGGTCTCGCTGGGAGAGAG	1139
Db	1191	ACCTGTCTTTTGGGAGCCACCACTTCCATGTGACGAAACAGGATCTGTATAGAGAGAG	1256
QY	1140	CCGAGACGACGAATGTGACGTCTGTGAGTCTTGTGCTCGGAAACTTACAGTGTGCCACAGA	1199
Db	1251	CCAGGAGAGTGAATGTGATGTCTGTGACCTTGGCTTGTGAAACTTACAGTGTGACGAGACGA	1310
QY	1200	CTTCTACTGCTGTGTCTCAAGATGATATTTAG 1233	
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RESULT 13	LOCUS	DEFINITION	VERSION	KEYWORDS
AK093427	AK093427	1867 bp	linear	
		Homo sapiens CDNA FLJ136108 f1s1, clone TESTR1201855, moderately similar to Mus musculus col1a1.interleukin-1 receptor 8 (TIR8) mRNA.		
ACCESSION	AK093427	AK093427.1	GI:21752294	
VERSION	AK093427	AK093427.1	GI:21752294	
KEYWORDS		oligo capping; f1s1 (full insert sequence).		

Db	1305	CCTGAAACCGGCCCGACCTGGCCCCCAGACCTCTTCTCCGATTTTGGAAAGAAATGC	1366
Oy	911	AGCTGGCCCTGCGCGGAAAGGTGCGCTACAGGCCGTGGAAAGAGA(CCCCCAGACGCAGC	970
Db	1365	AGCTGGCCCTCCCGGAAAGGTGCGGTACAGGCCGTGGAAAGGAAC(CCCCAAGACGCAGC	1424
Oy	971	TGCAGGAGCAGCAAGGACCCCATGTGTGATTTCTTCAGAGGCCAGAGTCCCTGAGGGCCGAGGCC	1033
Db	1425	TGCAGGAGCAGCAAGGACCCCATGTGTGATTTCTTCAGAGGCCAGATCCCTGAGGGCCGAGGCC	1488
Oy	1031	TGGA(CTCAGAGGTGAGCCCGGACCCCTTGAGGGCGAGCTTGAGTGTCCGGGGGCCCTGTATTTTG	1090
Db	1485	TGGA(CTCAGAGGTGAGCCCGGACCCCTTGAGGGCGAGCTTGAGTGTCCGGGGGCCCTGTATTTTG	1544
Oy	1091	GAGAGCCATCAGCTCCACCGCAGACCAATGGGGGTCCCTGGGAGAGCCGGAGACAGC	1155
Db	1545	GAGAGCCATCAGCTCCACCGCAGACCAATGGGGGTCCCTGGGAGAGCCGGAGACAGC	1604
Oy	1151	AAGTGAAGCTCTCGGATCTCGGCTTCGCAAACTACAGTGCCCGCAGACCTTCTTA(CTGCC	1210
Db	1605	AAGTGAAGCTCTCGGATCTCGGCTTCGCAAACTACAGTGCCCGCAGACCTTCTTA(CTGCC	1664
Oy	1211	TGGTGTCCAGAGATGATTTGAG	1233
Db	1665	TGGTGTCCAGAGATGATTTGAG	1687

QY	883	CCTTCCTCCGATTTTGGAAAGATGCAGCTGGGCTGCGCCGGAAAGCTGCGGTACAG	942
Db	551	CCTTCCTCCGATTTTGGAAAGATGCAGCTGGGCTGCGCCGGAAAGTGCAGTACAG	492
QY	943	CCGGTGAAGAGAGACCCCGACGCGCTGCAGAGACGAACAAGACCCCATGCTGATTC	1002
Db	491	CCTGTGAAGAGAGACCCCGACGCGCTGCAGAGACGAACAAGACCCCATGCTGATTC	432
QY	1003	CGAGGCCGATCTCTGAGGGCCGGGCTCTGATCTAGAGGTGGACCCGAACTGTAGGGC	1062
Db	431	CGAGGCCGATCTCTGAGGGCCGGGCTCTGATCTAGAGGTGGACCCGAACTGTAGGGC	372
QY	1063	GACCTGGGTGTCCGGGGGCTGTTTTGGAGAGCCATAGCTCCACCGCACACCAAGTGGG	1122
Db	371	GACCTGGGTGTCCGGGGGCTGTTTTGGAGAGCCATAGCTCCACCGCACACCAAGTGGG	312
QY	1123	GTCTTCGTGGAGAGAGCCGGAGCGACGAACTGGAATCTTGGAATCTTGCGTCCGGAAC	1182
Db	311	GTCTTCGTGGAGAGAGCCGGAGCGACGAACTGGAATCTTGGAATCTTGCGTCCGGAAC	252
QY	1183	TACAGTGCCCGACAGACTTCTACTGCTGTGTGCCAAGATGATATATAG	1233
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RESULT 14	BV177172/c	BV177172	655 bp	DNA	linear	STS 10-JUN-2004
LOCUS						
DEFINITION	sqgm93226 Human DNA (Sequenciom) Homo sapiens STS genomic, sequence tagged site.					
ACCESSION	BV177172					
VERSION	BV177172.1					
KEYWORDS	GI:4801190					
SOURCE	STS.					
ORGANISM	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 655)					
AUTHORS	Nelson,R.M., Marnellio,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.					
TITLE	Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions					
JOURNAL	Genome Res. (2004) In press					
COMMENT						

RESULT 15	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	FEATURES
AX525866	AX525866	Sequence 388 from Patent WO0206682.	AX525866	AX525866.1	GI:25170744			
							Rattus norvegicus (Norway rat)	
							Rattus norvegicus	
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
							1	
							Farris,G., Hicken,S.H. and Parr,S.B.	
							Rat toxicologically relevant genes and uses thereof	
							Patent: WO 0206682-A 388 2nd-AUG-2002;	
							Phase-1 Molecular Toxicology Inc. (US)	
							Location/Qualifiers	
							1..641	
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							/mol type="unassigned DNA"	

Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel.: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 655.

Location/Qualifiers

1. .655
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STS
ORIGIN

ORIGIN	Query Match	31.8%	Score 391.6;	DB 6;	Length 641;
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	Matches 454;	Conservative 0;	Mismatches 104;	Indels 0;	Gaps 0;
QY	673	ATCGTGGTCTTTTGGAGGCTTCTCTGAGCCGGGCTCTGTGCACACAGTTTCCGGAG	732		
DB	84	ATCGTGGTCTTTTAGATGCTTCTCAGAGTCTCTGTGTATACAGAGCTTCCGGAG	143		
QY	733	GGCGTGGCCGGGCTGTGAGCTCACCCGGCAGACCAATCTTCAATCACCTTGAGGGCAG	792		
DB	144	GGACTGTGCCGCTACTGAGACTACCCGGCAGACTTATCTTTATACACTTTCAGAGGCAG	203		
QY	793	AGGGCGACCCCGCGACCCGGGCGCTCGCTGTGTGGCGACACGGCACTGTGATCC	852		
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Query Match	32.3%	Score 398	DB 11	Length 655
Best Local Similarity	97.8%	Pred. No. 2.7e-52		
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		Gaps	0	
QY	823	CTGCTGGCCAGCACCCGCACTCTGTGTGACCTTGTCTCTCTGAGGCCCGGCTCCGTACT	882	
Db	611	CCGCTGCTGCGCAACCGCACCTGTATGACTCTGTGCTCTGTGAGAGCCCGGCTCCGTACT	552	

QY	853	CTGCTGCTCTGGAGAGCCCGGCTCCGTCATCTTCTCCATTTTGGAAAAGATGCAG	912
QY	264	CTGCTGCTCTGGAGAGCCCGGCTCCGTCATCTTCTCCATTTTGGAAAAGATGCAG	323
Db	913	CTGGCGCTGCCCGGAAAGTTCGGATACAGCCGGTGGAAAGAGAGACCCCTGACGACGCTG	972
QY	324	TTGGCACTACCACGAAAGGTGCATTAACAGACCCGTGGAGGAGAGACCCCTCAATCCGACTT	383

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QY 973 CAGGAGCAAGGACCCCATGCTGATTCTTCGAGGCCGAGTCCCTGAGGGCCGGGCGCTG 1032
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QY 1033 GACTCAGAGGTGAGCCCGGACCCCTGAGGGGGAACCTGGGTGTCCGGGGGCGCTGTTTGGGA 1092
Db 444 GAGTCAGAGGTGATCCAGACCCCTGAGGGGAGACCTGGGTGTCCGTGGACCTGTCTTGGG 503
QY 1093 GAGCCATCAGCTCCAGCGACACCAAGTGGGTCTCGCTGGGAGAGAGCCGAGAGCGAA 1152
Db 504 GAGCCACCAATCCACTACAGAAAGCAAGTCTCCATAGAGAGAGGCCATGCCAGTGAA 563
QY 1153 GTGGAGTCTCGGATCTCGGCTCGCGAAACTACAGTCCCGGACAGACTTCTACTGCGCTG 1212
Db 564 ATGGATGTCTTGACCTTGCGCTCTCGAACTACAGTGGCGGAACAGCTTCTACTGCGCTT 623
QY 1213 GTGCCAAGGATGATATG 1230
Db 624 GTGCTGAGGATGACGTG 641

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Search completed: July 30, 2005, 00:04:23
 Job time : 5666 secs

to identify human chromosome 11, to map genes on this chromosome and to identify disease-related genes (particularly in the region 11p15.5 where CC genes are present associated with e.g. arthropodis multiplex congenita, breast cancer, insulin-dependent diabetes, sickle cell CC anaemia, bladder cancer), including detection of defective genes; (c) to study cell-signal transduction and the SIGIRR system, and (d) in gene therapy. Sense and antisense oligonucleotides can be used to inhibit expression of the SIGIRR gene. The proteins of the invention are used: CC (i) to study cellular processes (immune regulation, proliferation, death, CC migration, interaction with other cells and inflammation); (ii) to CC identify and purify proteins that associate with SIGIRR ligands and CC receptors, and to measure their biological activity; (iii) in screening CC for, and rational design of, potential inhibitors of activity; (iv) therapeutically against diseases mediated by SIGIRR polypeptide counter-structures; (v) as molecular weight (m.w.) markers in electrophoresis; CC (vi) for determining isoelectric points of unknown proteins; (vii) as CC controls for determining the extent of protein fragmentation (e.g. to aid CC characterization of protein structures by mass spectrometry); (viii) for CC generation of antibodies (Ab); (ix) to deliver diagnostic or therapeutic CC agents to cells that express SIGIRR binding molecules

Sequence 1233 BP, 203 A, 408 C, 380 G, 242 T, 0 U, 0 Other:

Query Match 100.0%; Score 1233; DB 2; Length 1233;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGGCGCTCTTGAGGAGCTCAGTGGCTGTGATCTGACGCGCTTGAGGAGTCTTGAGGCC 120
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DB 121 CACTGCTCCCTGCTTCAGTCAAGTGGCTGAAAGACGGGCTTCATTGGAGATTTGGAGGC 180
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DB 301 CAGACATCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
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QY 781 TTGAGAGGCGAGAGGCGACACCCCGACCCGAGGCTCCGCTGTGCGGACGACCCG 840
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QY 841 CACTGTGTACCTTGTGCTCTGAGAGCGCGGCTCCGTAATCTTCTCCGATTTTGG 900
DB 841 CACTGTGTACCTTGTGCTCTGAGAGCGCGGCTCCGTAATCTTCTCCGATTTTGG 900
QY 901 AAGAGAGTACAGTGGCGTGGCGGAGAGTGGGATCAAGCGGAGTGAAGAGACCC 960
DB 901 AAGAGAGTACAGTGGCGTGGCGGAGAGTGGGATCAAGCGGAGTGAAGAGACCC 960
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QY 1021 GGCCTGGGCTTGGACTCAGAGGTGACCTCGGACCTTGAGGGGACCTTGAGGGG 1080
DB 1021 GGCCTGGGCTTGGACTCAGAGGTGACCTCGGACCTTGAGGGGACCTTGAGGGG 1080
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RESULT 2
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ID ADP54077 standard; cDNA; 1694 BP.
XX
AC ADP54077;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PRO cDNA sequence SEQ ID NO:53.
XX
DE human; PRO; immune related disease; inflammatory immune response;
XX immune response stimulation; antiallergic; antianemic; antiarthritic;
XX antidiabetic; antidiabetic; antidiabetic; antidiabetic;
XX antineoplastic; antineoplastic; CNS; dermatological; gastrointestinal;
XX haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
XX nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
XX virucide; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004039956-A2.
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PD 13-MAY-2004.
XX
PF 28-OCT-2003; 2003WO-US034381.
XX
PR 29-OCT-2002; 2002US-0422472P.
XX
PA (GENTH ) GENENTECH INC.
XX
PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
XX Wood WT, Wu TD;
XX WPI; 2004-376182/35.
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renal disease; demyelinating disease; central nervous system;
 peripheral nervous system; demyelinating polyneuropathy;
 Guillain-Barre syndrome;
 chronic inflammatory demyelinating polyneuropathy.
 Homo sapiens.
 WC200404361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
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 PA (GENTH) GENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WJ, Wu TD;
 XX
 DR WPI; 2004-420067/39.
 DR P-PSDB; ADOI9087.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS claim 1; SEQ ID NO 23; 1731bp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC hemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polynucleotide of
 CC the invention.
 CC
 XX
 XX
 Sequence 1695 BP; 329 A; 556 C; 510 G; 300 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1233; DB 12; Length 1695;
 Best Local Similarity 100.0%; Pred. No. 1.1e-236;
 Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GCGGTGCTGGCCCTCTCTGATGCTGAGCCCTGAGCTGAGGCGCCCTGCTATATG 420
 DB 587 GCGGTGCTGGCCCTCTCTGATGCTGAGCCCTGAGCTGAGGCGCCCTGCTATATG 646
 QY 421 AAGTCCGCTCAACGCTGCTGCTGATGCTGAGGCGCCCTGAGCTGAGGCGCCCTG 480
 DB 647 AAGTCCGCTCAACGCTGCTGCTGATGCTGAGGCGCCCTGAGCTGAGGCGCCCTG 706
 QY 481 GACGGAAAGCTCTACAGGCTGCTGATGCTGAGGCGCCCTGAGCTGAGGCGCCCTG 540
 DB 707 GACGGAAAGCTCTACAGGCTGCTGATGCTGAGGCGCCCTGAGCTGAGGCGCCCTG 766
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 DB 767 GTGAATTCATCTTAAAGCCGAGCTGAGGCGCCCTGAGCTGAGGCGCCCTGAGCT 826
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 DB 827 GACCGAGACCTCTGCGCGGCTGAGGCGCCCTGAGCTGAGGCGCCCTGAGCTGAG 886
 QY 661 TGCCGAGCCTCATGCTGCTGCTTGGAGGCTTCTTGAAGCCGCGCTGCTGAGCT 720
 DB 887 TGCCGAGCCTCATGCTGCTGCTTGGAGGCTTCTTGAAGCCGCGCTGCTGAGCT 946
 QY 721 AGCTTCGGGAGGCGCTGCTGCTGCTGAGGCTTCTTGAAGCCGCGCTGCTGAGCT 780
 DB 947 AGCTTCGGGAGGCGCTGCTGCTGCTGAGGCTTCTTGAAGCCGCGCTGCTGAGCT 1006
 QY 781 TTGAGGAGCAGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGCTGAGCTGAG 840
 DB 1007 TTGAGGAGCAGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGCTGAGCTGAG 1066
 QY 841 CACTGTGATCTTGTCTGCTGCTGAGGCGCGGAGCTGCTGAGCTGCTGAGCTGAG 900
 DB 1067 CACTGTGATCTTGTCTGCTGCTGAGGCGCGGAGCTGCTGAGCTGCTGAGCTGAG 1126
 QY 901 AAAGAATGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGCTGAGCTGAG 960
 DB 1127 AAAGAATGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGCTGAGCTGAG 1186
 QY 961 CAGAGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGCTGAGCTGAG 1020
 DB 1187 CAGAGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGCTGAGCTGAG 1246
 QY 1021 GCGCGGCGCTGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1080
 DB 1247 GCGCGGCGCTGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1306
 QY 1081 CCGTTTGGAGAGCCATGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1140
 DB 1307 CCGTTTGGAGAGCCATGAGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1366
 QY 1141 CGAGAGCAGAGGAGCTGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1200
 DB 1367 CGAGAGCAGAGGAGCTGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1426
 QY 1201 TTCTACTGCTGCTGCTGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1233
 DB 1427 TTCTACTGCTGCTGCTGCTGAGGCGCGGAGCCGCGGAGCTGCTGAGGCGCGCTGAG 1459

RESULT 5
 ADP22969 standard; cDNA; 1695 BP.
 XX
 XX ADP22969;
 AC
 XX
 DT 18-NOV-2004 (first entry)
 XX
 XX PRO polypeptide encoding cDNA SEQ ID NO:63.
 DE
 XX 88; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
 KM immunosuppressive; osteopathic; antidiabetic; dermatological;

KM antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
XX gene therapy; immune system.
OS unidentified.
XX WO2004041170-A2.
XX
XX 21-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-US034312.
XX
XX 01-NOV-2002; 2002US-0423394P.
XX
XX (GENTH) GENENTECH INC.
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX MPI; 2004-419628/39.
XX P-PSDB; ADP22970.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 1; SEQ ID NO 63; 2940bp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.
XX
XX
SQ Sequence 1695 BP; 329 A; 556 C; 510 G; 300 T; 0 U; 0 Other:
Query Match 100.0%; Score 1233; DB 13; Length 1695;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGAGGTGTCGTGATAGAGGCCCTGACTCTCTCCCGCTGAAGCAAGGTGCTG 60
DB ATGCGAGGTGTCGTGATAGAGGCCCTGACTCTCTCCCGCTGAAGCAAGGTGCTG 286
QY 61 AGGCGTCTTGGGAGAGCTCAGTGTCTCTGAACTGCAAGGCTTGGTGTCTGAGGCC 120
DB AGGCGTCTTGGGAGAGCTCAGTGTCTCTGAACTGCAAGGCTTGGTGTCTGAGGCC 346
QY 121 CACTGCTCCTGCTTCAAGTCAAGTGTGCTGAAGACGAGGCTTCAATTGGAGATTGGAGGC 180
DB CACTGCTCCTGCTTCAAGTCAAGTGTGCTGAAGACGAGGCTTCAATTGGAGATTGGAGGC 406

QY 181 CACTACAGCCTTCACAGAGTACTCTGGGTCAAGGCCCAACCTGTGACAGAGGTGTGTGCC 240
DB CACTACAGCCTTCACAGAGTACTCTGGGTCAAGGCCCAACCTGTGACAGAGGTGTGTGCC 466
QY 241 AGTGTCTTGGGGGTCAACGTGACCAAGCACTGAAGTCTATGGGGCTTCACTGTCTGCATC 300
DB AGTGTCTTGGGGGTCAACGTGACCAAGCACTGAAGTCTATGGGGCTTCACTGTCTGCATC 526
QY 301 CAGAACATCAGCTTCTCTCTCTTCACTCTTCAAGAGAGCTGGCCCTTCAAGCCACGTGGCT 360
DB CAGAACATCAGCTTCTCTCTCTTCACTCTTCAAGAGAGCTGGCCCTTCAAGCCACGTGGCT 586
QY 361 GCGGTGCTGGCCCTCTCTGTGTCGCTGGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB GCGGTGCTGGCCCTCTCTGTGTCGCTGGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
QY 421 AAGTGCCTGTCAACGTGTGCTGTGTACCAAGACGCTATGTGGAGGTGAGATTAAC 480
DB AAGTGCCTGTCAACGTGTGCTGTGTACCAAGACGCTATGTGGAGGTGAGATTAAC 706
QY 481 GACGGAGAGCTTACAGACGCTTACGTCTCTTACAGGAGATGCCCCGAGAGCCGCAAGTTC 540
DB GACGGAGAGCTTACAGACGCTTACGTCTCTTACAGGAGATGCCCCGAGAGCCGCAAGTTC 766
QY 541 GTGAACCTCATCTTAAAGCCGAGCTGAGCGGCGGTGGGGGTACAAAGCTCTTCTGAGAC 600
DB GTGAACCTCATCTTAAAGCCGAGCTGAGCGGCGGTGGGGGTACAAAGCTCTTCTGAGAC 826
QY 601 GACCGGAGCTTCTGCGCGCGCTGAGCCCTTCGCGGACCTTGTGTGAACCTGAGCCGC 660
DB GACCGGAGCTTCTGCGCGCGCTGAGCCCTTCGCGGACCTTGTGTGAACCTGAGCCGC 886
QY 661 TGGCCAGGCTCATGTGTGCTTTTGGAGCGCTTCTTGAAGCCGGGCTGTGTGACAGCCAC 720
DB TGGCCAGGCTCATGTGTGCTTTTGGAGCGCTTCTTGAAGCCGGGCTGTGTGACAGCCAC 946
QY 721 AGCTTCGGGAGAGGCGCTGTGCGGCTGTGAGTCAACCCGAGACCCATCTTCAATCAC 780
DB AGCTTCGGGAGAGGCGCTGTGCGGCTGTGAGTCAACCCGAGACCCATCTTCAATCAC 1006
QY 781 TTGAGAGGCGAGAGGCGGACCCCGGACCCGCGCTCCGCTGTGCGGACGACCCG 840
DB TTGAGAGGCGAGAGGCGGACCCCGGACCCGCGCTCCGCTGTGCGGACGACCCG 1066
QY 841 CACTGTGTAACTTGTGTGTGTGAGGCGGCGCTCGGTATCTTCTTCCGATTTTGG 900
DB CACTGTGTAACTTGTGTGTGTGAGGCGGCGCTCGGTATCTTCTTCCGATTTTGG 1126
QY 901 AAAGAAAGTCACTGGCGCTGCGCGGAGAGTGCAGGTCAGGCGGTTGAAGAGAGACCC 960
DB AAAGAAAGTCACTGGCGCTGCGCGGAGAGTGCAGGTCAGGCGGTTGAAGAGAGACCC 1186
QY 1127 AAAGAAAGTCACTGGCGCTGCGCGGAGAGTGCAGGTCAGGCGGTTGAAGAGAGACCC 1186
DB AAAGAAAGTCACTGGCGCTGCGCGGAGAGTGCAGGTCAGGCGGTTGAAGAGAGACCC 1246
QY 961 CAGACGCACTTCAAGACGACCAAGACCCCATGTGTATTTCTTGAAGCGGAGTCCCTGAG 1020
DB CAGACGCACTTCAAGACGACCAAGACCCCATGTGTATTTCTTGAAGCGGAGTCCCTGAG 1246
QY 1021 GGCCTGGGCTTGGATCTCAAGAGTGAACCGGACCTTGAAGGCGGACCTTGGGTGTCCGGGG 1080
DB GGCCTGGGCTTGGATCTCAAGAGTGAACCGGACCTTGAAGGCGGACCTTGGGTGTCCGGGG 1306
QY 1081 CCTGTTTTTGAAGAGCATCAGTCCACCGGACCAAGTGGGGTTCGCTGGAGAGAGC 1140
DB CCTGTTTTTGAAGAGCATCAGTCCACCGGACCAAGTGGGGTTCGCTGGAGAGAGC 1366
QY 1141 CGAGACAGGAAGTGAAGCTTTCGATCTCGGCTGCGAAACTTACAGTCCCGCACAGAC 1200
DB CGAGACAGGAAGTGAAGCTTTCGATCTCGGCTGCGAAACTTACAGTCCCGCACAGAC 1426
QY 1201 TTCTACTGCTGTGTGTCCAAAGATGATATGTAG 1233
DB TTCTACTGCTGTGTGTCCAAAGATGATATGTAG 1459

RESULT 6
AAFP27859
ID AAFP27859 standard; cDNA, 1659 BP.
XX
AC AAFP27859;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human NOV9 cDNA.
XX
KW Human; NOVX; antiinflammatory; cytoskeletal; neuroprotective;
KW cerebroprotective; immunomodulator; vulnereary; vasotropic; gene therapy;
KW hyperplasia; tumour; restenosis; psoriasis; Dupuytren's contracture;
KW diabetes; rheumatoid arthritis; cerebral oedema; Alzheimer's disease; ss.
XX
OS Homo sapiens.
XX
PN W0200075321-A2.
XX
PD 14-DEC-2000.
XX
PE 01-JUN-2000; 2000WO-US015303.
XX
PR 03-JUN-1999; 99US-0137332P.
PR 16-MAR-2000; 2000US-0189810P.
PR 22-MAR-2000; 2000US-0191158P.
PR 30-MAR-2000; 2000US-0193086P.
PR 31-MAY-2000; 2000US-00137322.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shlomo RA, Fernandes E, Herman J, Vernet C;
XX
DR WPI; 2001-102403/11.
XX
PT P-PSDB; AAB61137.
XX
PT New NOVX polypeptides and polynucleotides, useful in gene therapy, as a
PT diagnostic marker, protein therapeutic, antibody or small molecule drug
PT target for treating immune, proliferative and metabolic diseases and
PT wound healing.
XX
XX
PS Claim 8; Page 36-38; 194pp; English.
XX
CC The present sequence encodes a new isolated polypeptide (NOVX). The NOVX
CC polypeptides, NOVX nucleic acids, and anti-NOVX antibodies are useful for
CC treating or preventing NOVX-associated disorders. They are also useful
CC for determining the presence of or a predisposition to a disease
CC associated with altered levels of the NOVX polypeptide or nucleic acid.
CC These NOVX-associated disorders include hyperplasia, tumours,
CC restenosis, psoriasis, Dupuytren's contracture, diabetic complications,
CC rheumatoid arthritis, cerebral lesions, diabetic neuropathies, cerebral
CC oedema, senile dementia or Alzheimer's disease. The NOVX polynucleotides
CC are especially useful in gene therapy. Specifically, NOVX is useful as a
CC diagnostic marker or prognostic marker, protein therapeutic and antibody
CC target or small molecule drug target to treat disorders in the immune
CC response pathway, thyroid and metabolic diseases, bone metabolic
CC disorders, diseases of the pancreas (e.g. diabetes or digestive
CC disorders), proliferative diseases, or tissue regeneration and
CC development (e.g. wound healing or treatment of burns)
XX
SQ Sequence 1659 BP; 296 A; 551 C; 504 G; 308 T; 0 U; 0 Other;
Query Match 99.9%; Score 1231.4; DB 4; Length 1659;
Best Local Similarity 99.9%; Pred. No. 2.3e-236;
Matches 1232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCCAGGTGTCTGTATAGGAGCCCTGACTTCTCTCCCGTGTGAAGACCAAGTCTGT 60
DB 244 ATGCCAGGTGTCTGTATAGGAGCCCTGACTTCTCTCCCGTGTGAAGACCAAGTCTGT 303
QY 61 AGGCTGCTTGGGACCTGAGTGTCTGTGAACGTGACGGCTTGGGAGTCTCTGGGGCC 120

DB 304 AGGCTGCTTGGGACCTGAGTGTCTGTGAACGTGACGGCTTGGGAGTCTCTGGGGCC 363
QY 121 CACTGTCCCTGCTTCAATGCTGAGTGTGAAAGACGGGCTTCCATTGGGAAATGGGGG 180
DB 364 CACTGTCCCTGCTTCAATGCTGAGTGTGAAAGACGGGCTTCCATTGGGAAATGGGGG 423
QY 181 CACTGACAGCTTCCAGAGTACTCTGTGGTCAAGGCAACCTGTGAGAGGTCTGTGTCC 240
DB 424 CACTGACAGCTTCCAGAGTACTCTGTGGTCAAGGCAACCTGTGAGAGGTCTGTGTCC 483
QY 241 AGTGTCTGGGGGCTCAAGTGTGACGAGCACTGAATGATGAGGAGCTTCACTGTCTCATC 300
DB 484 AGTGTCTGGGGGCTCAAGTGTGACGAGCACTGAATGATGAGGAGCTTCACTGTCTCATC 543
QY 301 CAGAACATCAGCTTCT 360
DB 544 CAGAACATCAGCTTCT 603
QY 361 GCGGTGTGGGCTTCCCT 420
DB 604 GCGGTGTGGGCTTCCCT 663
QY 421 AAGTGTCTGCTCAAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 664 AAGTGTCTGCTCAAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 723
QY 481 GACGGGAAGCTTACGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 724 GACGGGAAGCTTACGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 783
QY 541 GTGAATCTTCAATCTTAAAGCCGAGCTGAGAGCGGTGTGGGGCTTCAAGCTTCTCTGAC 600
DB 784 GTGAATCTTCAATCTTAAAGCCGAGCTGAGAGCGGTGTGGGGCTTCAAGCTTCTCTGAC 843
QY 601 GACCGGACCTTCTGCGCGGCTGAGCGCTGAGCGCGGCTTCTGAGGAACTGTAGCGCG 660
DB 844 GACCGGACCTTCTGCGCGGCTGAGCGCTGAGCGCGGCTTCTGAGGAACTGTAGCGCG 903
QY 661 TGCCGAGCTTCAATCTGAGTGTCTTGTGAGCGCTTCTGAGCGCGGCTTGTGAGCGCAC 720
DB 904 TGCCGAGCTTCAATCTGAGTGTCTTGTGAGCGCTTGTGAGCGCGGCTTGTGAGCGCAC 963
QY 721 AGCTTCCGGAGGAGCGCTGTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 964 AGCTTCCGGAGGAGCGCTGTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1023
QY 781 TTGAGAGGCGAGAGGAGCGGACCCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 840
DB 1024 TTGAGAGGCGAGAGGAGCGGACCCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1083
QY 841 CACTGTGTGACTTGTGTCTGT 900
DB 1084 CACTGTGTGACTTGTGTCTGT 1143
QY 901 AAAGAATGTGAGT 960
DB 1144 AAAGAATGTGAGT 1203
QY 961 CAGAGCGAGCTGAGAGGAGCAAGAGACCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 1204 CAGAGCGAGCTGAGAGGAGCAAGAGACCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1263
QY 1021 GGCAGGAGCTTGTGAGT 1080
DB 1264 GGCAGGAGCTTGTGAGT 1323
QY 1081 CTTGT 1140
DB 1324 CTTGT 1383
QY 1141 CGAGAGCAGAGT 1200
DB 1384 CGAGAGCAGAGT 1443

QY 1201 TTCTACTGCTGCTGTCCTCAAGATGATATAG 1233
DB 1444 TTCTACTGCTGCTGTCCTCAAGATGATATAG 1476

RESULT 7
ACD40262
ID ACD40262 standard; DNA; 1659 BP.

AC ACD40262;
XX
XX
DT 03-SEP-2003 (first entry)
XX
XX
DE Human breast tumour associated protein 47-like polypeptide NOV4 DNA.

XX Tissue typing; cancer; breast cancer; colon cancer; lung cancer; sarcoma;
XX pancreatic cancer; uterine cancer; organ transplantation disorder; ds;
XX cardiovascular disease; melanoma; atherosclerosis; diabetes mellitus;
XX ischaemic heart disease; haemorrhage; peripheral vascular disease; gene;
XX thrombosis; hypertension; systemic lupus erythematosus; haematopoiesis;
XX tissue regeneration; wound healing; hyperproliferative disorder;
XX psoriasis; neural disorder; Parkinson's disease; Alzheimer's disease;
XX Huntington's disease; multiple sclerosis; amyotrophic lateral sclerosis;
XX ALS; peripheral neuropathy; nervous system tumour; neurotoxin; tremor;
XX neuropathy; acute brain injury; peripheral nerve trauma; human; NOVX;
XX gene therapy; epilepsy; breast tumour associated protein 47.

XX Homo sapiens.
OS
XX US2003027158-A1.
XX
XX PD 06-FEB-2003.
XX
XX 15-OCT-2001; 2001US-00977418.
XX
XX PF 03-JUN-1999; 99US-0137322P.
XX PR 16-MAR-2000; 2000US-0189810P.
XX PR 22-MAR-2000; 2000US-0191158P.
XX PR 30-MAR-2000; 2000US-0193086P.
XX PR 03-MAY-2000; 2000US-0201388P.
XX PR 31-MAY-2000; 2000US-00584411.
XX
XX
XX (CURA-) CURAGEN CORP.
XX
XX PI Shimketa RA, Fernandez E, Herrman J, Vernet C;
XX
XX DR MPI; 2003-492028/46.
XX DR P-SDB; ABO23241.
XX
XX PT New nucleic acid sequence encoding a human breast tumor-associated
XX protein 47-like polypeptide, useful for treating cardiovascular
XX disorders, neural disorders, diabetes mellitus and cancers.
XX
XX PS Disclosure; Page 23-25; 100p; English.

XX The invention relates to a new isolated NOV4 nucleic acid. The nucleic
XX acid is useful for identifying a compound that binds the nucleic acid.
XX The nucleic acid is useful in gene therapy, in screening assays, in
XX detection assays e.g. chromosomal mapping, cell and tissue typing and
XX forensic biology, predictive medicine e.g. diagnostic assays, prognostic
XX assays, monitoring clinical trials and pharmacogenomics and methods of
XX treatment including therapeutic and prophylactic. The nucleic acid is
XX also useful for expressing NOVX protein. The nucleic acid is also useful
XX to provide polynucleotide reagents e.g. labelled probes that are useful
XX in an in situ hybridisation technique, for identifying a specific class
XX (for example brain tissue) and for use in forensic science. The nucleic
XX acid is also useful for mapping genes on a chromosome and thus locating
XX gene regions associated with genetic disease, identifying an individual
XX from a minute biological sample and to aid in forensic identification of
XX biological sample. The nucleic acid is also useful for treating cancer,
XX especially cancers of the breast, colon, lung, pancreas or uterus, or a
XX melanoma or sarcoma. The nucleic acid is also useful for treating

CC disorders related to organ transplantation, cardiovascular diseases,
CC atherosclerosis, ischaemic heart disease, haemorrhage, diabetes mellitus,
CC peripheral vascular disease, thrombosis, hypertension and systemic lupus
CC erythematosus. NOVX protein encoded by the nucleic acid is useful for
CC regulating haematopoiesis, for regeneration of bone, cartilage, tendon
CC ligament and/or nerve tissue growth or regeneration and for wound
CC healing. The nucleic acid is also useful for treating infections,
CC hyperproliferative disorders e.g. psoriasis, and neural disorders
CC including Parkinson's disease, Alzheimer's disease, Huntington's disease,
CC multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral
CC neuropathy, tumours of the nervous system, exposure to neurotoxins, acute
CC brain injury, peripheral nerve trauma or injury and other neuropathies,
CC epilepsy, and/or tremors. The present sequence represents DNA encoding a
CC human breast tumour associated protein 47-like polypeptide
XX
XX
SQ Sequence 1659 BP; 295 A; 552 C; 504 G; 308 T; 0 U; 0 Other;

Query Match 99.9%; Score 1231.4; DB 9; Length 1659;
Best Local Similarity 99.9%; Pred. No. 2,3e-236;
Matches 1232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCAGGTGTCTGTGATATAGGCCCCCTGACTTCTCCCGCTTGAAGACCAAGTGTCTG 60
DB 244 ATGCCAGGTGTCTGTGATATAGGCCCCCTGACTTCTCCCGCTTGAAGACCAAGTGTCTG 303
QY 61 AGGCGTGCCTTGGGGGACGCTCAAGTGTCTGAACTGACAGGCTTGGGTAAGTCTTGGGCCC 120
DB 304 AGGCGTGCCTTGGGGGACGCTCAAGTGTCTGAACTGACAGGCTTGGGTAAGTCTTGGGCCC 363
QY 121 CACTGTCTCCCTGCTTCACTTCAGTCCAGTGGCTGAAAGACGGGCTTTCATTGGGAAATTTGGGGCC 180
DB 364 CACTGTCTCCCTGCTTCACTTCAGTCCAGTGGCTGAAAGACGGGCTTTCATTGGGAAATTTGGGGCC 423
QY 181 CACTACAGGCTTCAAGAGTATCTCTTGGGTCAGGCCCCAACCCTGTCANAGGTCTTGTGTCC 240
DB 424 CACTACAGGCTTCAAGAGTATCTCTTGGGTCAGGCCCCAACCCTGTCANAGGTCTTGTGTCC 483
QY 241 AGTGTCTTGGGGGTCACAGTGTACACAGCACTGAAATCTATGGGGCTTTCACCTGCTCATC 300
DB 484 AGTGTCTTGGGGGTCACAGTGTACACAGCACTGAAATCTATGGGGCTTTCACCTGCTCATC 543
QY 301 CAGAACATGAGCTTCTCTCTCTTCACTCTTCAGAGAGCTGGCCCTTCAAGCCACGTGGCT 360
DB 544 CAGAACATGAGCTTCTCTCTCTTCACTCTTCAGAGAGCTGGCCCTTCAAGCCACGTGGCT 603
QY 361 GCGGTCTGTGCT 420
DB 604 GCGGTCTGTGCT 663
QY 421 AAGTGCCTCTCAACGTCGCTCTGTATCAAGAGCGCGTATGGGAGGTGAGATTAAC 480
DB 664 AAGTGCCTCTCAACGTCGCTCTGTATCAAGAGCGCGTATGGGAGGTGAGATTAAC 723
QY 481 GACGGGAAGCTTACAGACGCTTACGTCCTCTCAAGGACTGCCCGAGAGCCGCAAGTTTC 540
DB 724 GACGGGAAGCTTACAGACGCTTACGTCCTCTCAAGGACTGCCCGAGAGCCGCAAGTTTC 783
QY 541 GTGAATTTATCTTAAGCGCGACGCTGTGAGCGGCTGTGGGGCTTCAAGCTCTTCTGTGAC 600
DB 784 GTGAATTTATCTTAAGCGCGACGCTGTGAGCGGCTGTGGGGCTTCAAGCTCTTCTGTGAC 843
QY 601 GACCGGACCTCTGTGCGCGGCTGAGCCCTCGCGGACCTCTTGTGAACTGTAGCGCG 660
DB 844 GACCGGACCTCTGTGCGCGGCTGAGCCCTCGCGGACCTCTTGTGAACTGTAGCGCG 903
QY 661 TGGCGAGCGCTCATCGTGTGCTTTTGGAGCGCTTCTTGAAGCGGAGCTGTGACGAC 720
DB 904 TGGCGAGCGCTCATCGTGTGCTTTTGGAGCGCTTCTTGAAGCGGAGCTGTGACGAC 963
QY 721 AGCTTCCGGGAGGGGCTGTGCGGCTGTGAGACTTACCGGAGACCCATCTTCAATAC 780
DB 964 AGCTTCCGGGAGGGGCTGTGCGGCTGTGAGACTTACCGGAGACCCATCTTCAATAC 1023

Qy 781 TTCCAGGGCCAGAGGCGGACCCCGGCGCTCCGCTGCTGGCCAGACCCG 840
Db 1024 TTCCAGGGCCAGAGGCGGACCCCGGCGCTCCGCTGCTGGCCAGACCCG 1083
Qy 841 CACCTGGTGAACCTTGTCTGTCTGGAAGCCCGGCTCCGTAATCTTCCGATTTTGG 900
Db 1084 CACCTGGTGAACCTTGTCTGTCTGGAAGCCCGGCTCCGTAATCTTCCGATTTTGG 1143
Qy 901 AAAAAGTGCAGCTGCGCTCCCGGGAAGGTGCGGTACAGCCGCGTGAAGAGACCC 960
Db 1144 AAAAAGTGCAGCTGCGCTCCCGGGAAGGTGCGGTACAGCCGCGTGAAGAGACCC 1203
Qy 961 CAGACGAGCTGCAAGAGCAAGAGACCCCAATGCTATTCTTCAAGGCGGAGTCCCTGAG 1020
Db 1204 CAGACGAGCTGCAAGAGCAAGAGACCCCAATGCTATTCTTCAAGGCGGAGTCCCTGAG 1263
Qy 1021 GGGCGGGGCTTGAAGCTCAAGAGTGAAGCCCGGACCTTGAGGGCGACCTGGTGTCCGGGG 1080
Db 1264 GGGCGGGGCTTGAAGCTCAAGAGTGAAGCCCGGACCTTGAGGGCGACCTGGTGTCCGGGG 1323
Qy 1081 CTTGTTTTTGGAGAGCCATCACTTCACCCGACACCACTGGGGGTCTGCTGGAGAGAGC 1140
Db 1324 CTTGTTTTTGGAGAGCCATCACTTCACCCGACACCACTGGGGGTCTGCTGGAGAGAGC 1383
Qy 1141 CGAGAGCGAAGTGAAGTCTCGGATCTCGGGAATCTACAGTGCCTGGACAGAC 1200
Db 1384 CGAGAGCGAAGTGAAGTCTCGGATCTCGGGAATCTACAGTGCCTGGACAGAC 1443
Qy 1201 TTCTACTGCTGTGTCTCAAGATGATATGTAG 1233
Db 1444 TTCTACTGCTGTGTCTCAAGATGATATGTAG 1476

RESULT 8
ADM56382
ID ADM56382 standard; cDNA; 1659 BP.

XX

AC ADM56382;

DT 03-JUN-2004 (first entry)

DE Human cDNA encoding cell adhesion molecule NOVX.

XX Human; BB; Gene; cell adhesion molecule; NOVX; cancer; leukemia;

KM lymphoma; melanoma; neurological disorder; epilepsy;

KM ischemic cerebrovascular disease; stroke; Alzheimer's disease;

KM Pick's disease; vesicular transport disorder; cystic fibrosis;

KM diabetes mellitus; Grave's disease; goiter; gastrointestinal disorder;

KM ulcerative colitis; gastric ulcer; duodenal disorder; autoimmune disease;

KM allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis;

KM viral infection; bacterial infection; fungal infection;

KM helminthic infection; protozoal infections.

XX Homo sapiens.

OS US2003082554-A1.

PN 01-MAY-2003.

XX 15-OCT-2001; 2001US-00977033.

XX 03-JUN-1999; 99US-0137322P.

PR 16-MAR-2000; 2000US-019810P.

PR 22-MAR-2000; 2000US-0191158P.

PR 30-MAR-2000; 2000US-0193086P.

PR 03-MAY-2000; 2000US-0201388P.

PR 31-MAY-2000; 2000US-00584411.

XX (CURA-) CURAGEN CORP.

PA Shinkets RA, Fernandes E, Herrman J, Vernet C;

PI WPI, 2003-616079/58.

DR P-PSDB; ADM56381.

XX New nucleic acids encoding human cell adhesion molecule-like proteins,

PT useful for treating e.g. cancers, neurological disorders, viral,

PT bacterial, fungal, helminthic and protozoal infections.

XX Example 6; SEQ ID NO 17; 76bp; English.

XX The invention relates to an isolated nucleic acid encoding a human cell

CC adhesion molecule-like protein, comprising a sequence encoding a

CC polypeptide having a sequence appearing as ADM56387, a sequence at least

CC 90% identical to the nucleic acid, a sequence encoding a polypeptide

CC having conservative amino acid substitutions to the protein or a fragment

CC comprising at least 20 nucleotides. Also included are an oligonucleotide

CC sequence that is complementary to (and hybridises under stringent

CC conditions with) the nucleic acid, a cell comprising the vector, a

CC pharmaceutical composition comprising the nucleic acid and a

CC pharmaceutical carrier, a process for producing the polypeptide, a

CC process for identifying a compound that binds the nucleic acid, and a

CC compound identified by the process. Disclosed as new are the cDNA and

CC proteins for novel cell adhesion molecules (termed NOVX, being NOV1-23).

CC The NOVX polypeptide, nucleic acid or antibody are useful in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease selected from NOVX-associated disorder, such as cancers

CC (e.g. leukemia, lymphoma, melanoma or cancer of the liver, lung, muscle,

CC ovary, testis and uterus), neurological disorders (e.g. epilepsy, Pick's

CC disease), disorders of vesicular transport (e.g. cystic fibrosis,

CC diabetes mellitus, Grave's disease, or goiter), gastrointestinal

CC disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),

CC autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic

CC anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic

CC and protozoal infections. The polypeptides can be used as immunogens to

CC produce antibodies and as vaccines. The sequences may further be used in

CC chromosome mapping, identifying individual from minute biological samples

CC (tissue typing), and in forensic identification of a biological sample.

CC NOTE: The authors have mis-labelled the sequences as they appear on pages

CC 12-28 of the patent, it is clear from table 3, the examples and the

CC claims that the SEQ ID numbers for the cDNAs should be the odd numbers

CC from 1-45 and the proteins should be the even numbers from 2-46. The

CC present sequence encodes a NOVX cell adhesion molecule of the invention.

XX

XX Sequence 1659 BP; 296 A; 551 C; 504 G; 308 T; 0 U; 0 Other;

XX Query Match 99.9%; Score 1231.4; DB 11; Length 1659;

XX Best Local Similarity 99.9%; Pred. No. 2.3e-236;

XX Matches 1232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCAGGTGTCTGTATGAGGCGCCCTGACTTCTTCCCGGTGTAAGACAGGTGCTG 60

Db 244 ATGCCAGGTGTCTGTATGAGGCGCCCTGACTTCTTCCCGGTGTAAGACAGGTGCTG 303

Qy 61 AGGCGTGGCTTGGGACCTGAGTGGCTGTAAGTGAAGCGGCTTGGAGTCTGGGGCC 120

Db 304 AGGCGTGGCTTGGGACCTGAGTGGCTGTAAGTGAAGCGGCTTGGAGTCTGGGGCC 363

Qy 121 CACTGCTCCCTGCTTCACTGAGTGAAGACCGGCTTCCATTGGGAAATTTGGGGC 180

Db 364 CACTGCTCCCTGCTTCACTGAGTGAAGACCGGCTTCCATTGGGAAATTTGGGGC 423

Qy 181 CACTACAGCTTCCACGAGTACTCTGGGTCAAGGCCAAGCTGTGAGGTGTGTGTC 240

Db 424 CACTACAGCTTCCACGAGTACTCTGGGTCAAGGCCAAGCTGTGAGGTGTGTGTC 483

Qy 241 AGTGTCTGGGGGGTCAAGGACGACGAGTGAAGTCAATGAGGGCTTCACTGTCATC 300

Db 484 AGTGTCTGGGGGGTCAAGGACGACGAGTGAAGTCAATGAGGGCTTCACTGTCATC 543

Qy 301 CAGAACATCAGCTTCTTCTCTTCACTTCAAGAGACTGACCTCAAGCAAGTGGCT 360

Db 544 CAGAACATCAGCTTCTTCTCTTCACTTCAAGAGACTGACCTCAAGCAAGTGGCT 603

PT Novel substantially purified NOVX polypeptide for treating severe
PT combined immunodeficiency, candidiasis, cancer, asthma, multiple
PT sclerostis, systemic lupus erythematosus.
XX
PS Disclosure; SEQ ID NO 17, 155bp; English.
XX
CC The invention relates to human NOVX polypeptides and polynucleotides.
CC NOVX sequences are useful in the treatment of cancer, hyperproliferative
CC diseases, cirrhosis, keloid, psoriasis, tissue hypertrophy,
CC osteoarthritis, atherosclerotic plaque formation, haemorrhage, ischaemic
CC heart or renal disease, thrombosis, diabetes mellitus, hypertension,
CC hypohydridism, aschma, burns, incisions, ulcers, periodontal disease,
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, Shy-Drager syndrome, immune deficiencies
CC and disorders such as severe combined immunodeficiency (SCID), bacterial
CC infection, viral infection e.g. herpes viral infection, protozoan
CC infection e.g. malaria, fungal infection e.g. candidiasis, autoimmune
CC disorders such as connective tissue disease, multiple sclerosis, systemic
CC lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary
CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin
CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
CC and autoimmune inflammatory eye disease. The invention is useful in
CC regeneration and tissue growth of bone, cartilage, tendon, ligament,
CC haematopoiesis regulation, wound healing and tissue repair. Sequences of
CC the invention also exhibit antitumor and antiinflammatory activities. The
CC present sequence is human NOVX DNA.
XX
XX

Seq Sequence 1659 BP; 296 A; 551 C; 504 G; 308 T; 0 U; 0 Other;

Query Match 99.9%; Score 1231.4; DB 12; Length 1659;
Best Local Similarity 99.9%; Pred. No. 2.3e-236;
Matches 1232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCAGTGTCTGTATAGAGGCCCTGAATCTCTCCCTGTAAGACAGTGTCTG 60
DB 244 ATGCCAGTGTCTGTATAGAGGCCCTGAATCTCTCCCTGTAAGACAGTGTCTG 303
QY 61 AGGCTGAGCTTTGGGAGAGCTCAGTGTCTGTAAGCTGACGAGCTTGGAGGCC 120
DB 304 AGGCTGAGCTTTGGGAGAGCTCAGTGTCTGTAAGCTGACGAGCTTGGAGGCC 363
QY 121 CACTGTCTCTGCTTCAGTCAAGTGTGTAAGAGCGAGCTTCATTGGAGATTTGGAGGC 180
DB 364 CACTGTCTCTGCTTCAGTCAAGTGTGTAAGAGCGAGCTTCATTGGAGATTTGGAGGC 423
QY 181 CACTACAGCTTCCACAGATATCTCTGGGTCAAGGCCAATCTGTCAGAGTGTGTGTCC 240
DB 424 CACTACAGCTTCCACAGATATCTCTGGGTCAAGGCCAATCTGTCAGAGTGTGTGTCC 483
QY 241 AGTGTCTGGGGGTCAAGCTGACAGCACTGAAGTATATGGAGCTTCACTGCTCATC 300
DB 484 AGTGTCTGGGGGTCAAGCTGACAGCACTGAAGTATATGGAGCTTCACTGCTCATC 543
QY 301 CAGAACATCAGCTTCTCTCTCTTCACTTTCAGAGAGCTGGCTCAAGCCAGCTGTGCT 360
DB 544 CAGAACATCAGCTTCTCTCTCTTCACTTTCAGAGAGCTGGCTCAAGCCAGCTGTGCT 603
QY 361 GCGGTGTGGAGCTTCT 420
DB 604 GCGGTGTGGAGCTTCT 663
QY 421 AAGTGCCTGCTCAACAGTGTCTCTGTAACAGAGCGATATGGAGAGTGAATTAAC 480
DB 664 AAGTGCCTGCTCAACAGTGTCTCTGTAACAGAGCGATATGGAGAGTGAATTAAC 723
QY 481 GACGGGAAGCTCTACGAGCGCTTACGTCTCTTACAGCACTGCCCGAGAGCGCAAGTTC 540
DB 724 GACGGGAAGCTCTACGAGCGCTTACGTCTCTTACAGCACTGCCCGAGAGCGCAAGTTC 783
QY 541 GTGAACCTTATCTTAAGCGGAGCTGGAGCGGAGCTGGAGCTTCAAGCTTCTCTGAGC 600
DB 784 GTGAACCTTATCTTAAGCGGAGCTGGAGCGGAGCTGGAGCTTCAAGCTTCTCTGAGC 843

QY 601 GACCGGACCTCTGCGCGCGCTGAGCCCTCCGCGACCTCTGTGTAACCTGAGCCGC 660
DB 844 GACCGGACCTCTGCGCGCGCTGAGCCCTCCGCGACCTCTGTGTAACCTGAGCCGC 903
QY 661 TGGCGAGCTCTATCTGTGTCTTTTCGAGAGCGCTTCTGAGCCCGAGCTGTGTGACGC 720
DB 904 TGGCGAGCTCTATCTGTGTCTTTTCGAGAGCGCTTCTGAGCCCGAGCTGTGTGACGC 963
QY 721 AGCTTCCGGGAAGGCGCTGTGCGCGCTGTGAGTCTACCGGAGACCACTTCACTACCC 780
DB 964 AGCTTCCGGGAAGGCGCTGTGCGCGCTGTGAGTCTACCGGAGACCACTTCACTACCC 1023
QY 781 TTGAGAGGCGAGAGGCGCAGCCCGCGAGCCCGCGCTCTGCTGTGCGCAGCAGCCGC 840
DB 1024 TTGAGAGGCGAGAGGCGCAGCCCGCGAGCCCGCGCTCTGCTGTGCGCAGCAGCCGC 1083
QY 841 CACTGTGTACCTTGTCTCTGTGAGAGCCCGCTCCGTGATCTCTTCCGATTTTGTG 900
DB 1084 CACTGTGTACCTTGTCTCTGTGAGAGCCCGCTCCGTGATCTCTTCCGATTTTGTG 1143
QY 901 AAAAGAGTACAGTGTGCGCTGCGCGAGAGTGTGCGTACAGGCGGAGAGAGAGCCGC 960
DB 1144 AAAAGAGTACAGTGTGCGCTGCGCGAGAGTGTGCGTACAGGCGGAGAGAGAGCCGC 1203
QY 961 CAGACGCACTGTCAGAGCAGCAAGAGACCCCATGTGATTTCTTGAAGCCGAGTCCCTGAG 1020
DB 1204 CAGACGCACTGTCAGAGCAGCAAGAGACCCCATGTGATTTCTTGAAGCCGAGTCCCTGAG 1263
QY 1021 GGGCGGGGCTTGTGATCTCAGAGTGTGACCCGAGACCTGAGGAGGAGACTTGGGTGTCCGGGG 1080
DB 1264 GGGCGGGGCTTGTGATCTCAGAGTGTGACCCGAGACCTGAGGAGGAGACTTGGGTGTCCGGGG 1323
QY 1081 CCGTTTTTTGAGAGGCACTCAGTCCACGCGACACAGAGTGGGGTCTCGCTGGAGAGAGAG 1140
DB 1324 CCGTTTTTTGAGAGGCACTCAGTCCACGCGACACAGAGTGGGGTCTCGCTGGAGAGAGAG 1383
QY 1141 CGAGCAGCGAAGTGTGACGCTCTCGATCTCGGCTCGCGAAATCAAGTCCCGCAGAGAC 1200
DB 1384 CGAGCAGCGAAGTGTGACGCTCTCGATCTCGGCTCGCGAAATCAAGTCCCGCAGAGAC 1443
QY 1201 TTCTACTGCTGTGTGTCTCAAGATGATATGTAG 1233
DB 1444 TTCTACTGCTGTGTGTCTCAAGATGATATGTAG 1476

RESULT 11
AD119781
ID AD119781 standard; DNA; 1659 BP.
XX
AC AD119781;
XX
DT 22-APR-2004 (first entry)
XX
XX Human NOV9 DNA.
DE
XX
XX Secreted protein; NOVX; diagnosis; metabolic disorder; diabetes; obesity;
XX infection; anorexia; cancer; cardiovascular disease; hypertension;
XX atherosclerosis; neurodegenerative disorder; Alzheimer's disease;
XX Parkinson's disease; epilepsy; immune disorder; osteoarthritis;
XX haematopoietic disorder; inflammatory skin disorder; asthma;
XX dyslipidemia; neurogenesis; cell differentiation; cell proliferation;
XX haematopoiesis; wound healing; angiogenesis; chromosome mapping;
XX tissue typing; preventive medicine; pharmacogenomic; gene therapy;
XX anorectic; cardiac; vincicide; antibacterial; fungicide; protozoacide;
XX neotropic; neuroprotective; dermatological; human; gene; db.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 244..1476
FT /tag= a
FT /product= "Human NOV protein"
FT /transl_except= (pos352..354, aa:Val)

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XX US2004002134-A1.
PN
XX
PD 01-JAN-2004.
XX
PF 15-OCT-2001; 2001US-00977819.
XX
PR 03-JUN-1999; 99US-0137322P.
PR 16-MAR-2000; 2000US-0189810P.
PR 22-MAR-2000; 2000US-0191158P.
PR 30-MAR-2000; 2000US-0193086P.
PR 03-MAY-2000; 2000US-0201388P.
PR 31-MAY-2000; 2000US-00584411.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkete RA, Fernandes ER, Herrman JL, Vernet CM;
PT WPI; 2004-070737/07.
DR P-PSDB; ADI19782.
XX
PT New NOVX nucleic acids encoding human KIAA0768 protein-like and human
PT protein PRO-228 polypeptides, useful for treating NOVX-associated
PT disorders.
XX
PS Disclosure; SEQ ID NO 17; 95pp; English.
XX
CC The present invention is based in part on the discovery of novel secreted
CC and membrane-bound polypeptides and their encoding polynucleotides. The
CC nucleic acids and polypeptides are collectively referred as NOVX. The
CC invention is useful for treating, preventing and diagnosing diseases such
CC as metabolic disorders, diabetes, obesity, infectious diseases such as
CC viral, bacterial, fungal, helminthic and protozoal infections, anorexia,
CC cancer, cardiovascular diseases such as hypertension and atherosclerosis,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC epilepsy, immune disorders such as osteoarthritis, haematopoietic
CC disorders, inflammatory skin disorders, asthma and various dyslipidemias.
CC The invention is also useful as targets for the identification of small
CC molecules that modulate or inhibit e.g. neurogenesis, cell
CC differentiation, cell proliferation, haematopoiesis, wound healing and
CC angiogenesis, as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine and pharmacogenomics. The invention is also
CC useful in gene therapy. The present sequence is human NOV DNA.
XX
SQ Sequence 1659 BP; 295 A; 552 C; 502 G; 308 T; 0 U; 2 Other;
Query Match 99.8%; Score 1230.4; DB 12; Length 1659;
Best Local Similarity 99.8%; Pred. No. 3,7e-236;
Matches 1231; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCCAGGTGTCTGTATAGAGGCCCTGACTTCTCTCCCGTCTGAAGCAAGTGTCTG 60
DB 244 ATCCCAAGTGTCTGTATAGAGGCCCTGACTTCTCTCCCGTCTGAAGCAAGTGTCTG 303
QY 61 AGGCGTGGCTTTGGAGAGCTAGTGTCTGAAGCTGCAAGCGGCTTGGTGAAGTCTGGGCCC 120
DB 304 AGGCGTGGCTTTGGAGAGCTAGTGTCTGAAGCTGCAAGCGGCTTGGTGAAGTCTGGGCCC 363
QY 121 CACTGTCTCTGCTTCACTCAGTGTGCTGAAGAAGCGGCTTCAATTGGAGATTGGGGGGC 180
DB 364 CACTGTCTCTGCTTCACTCAGTGTGCTGAAGAAGCGGCTTCAATTGGAGATTGGGGGGC 423
QY 181 CACTACAGCTTCAAGAGTACTCTGGGTCAAGGCCAACTGTCAAGAGTGTGTGTCC 240
DB 424 CACTACAGCTTCAAGAGTACTCTGGGTCAAGGCCAACTGTCAAGAGTGTGTGTCC 483
QY 241 AGTGTCTGGGGGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 300
DB 484 AGTGTCTGGGGGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 543
QY 301 CAGAACATCAGCTTCTCTCTCTCACTTCAAGAGAGTGGCCCTCAAGCCAGCTGTGCT 360
DB 544 CAGAACATCAGCTTCTCTCTCTCTCACTTCAAGAGAGTGGCCCTCAAGCCAGCTGTGCT 603
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QY 361 GCGGTGTGGCTTCCCTCTCTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 420
DB 604 GCGGTGTGGCTTCCCTCTCTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 663
QY 421 AAGTCCGTCTCAACAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 480
DB 664 AAGTCCGTCTCAACAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 723
QY 481 GACGGAGAGCTTCAACAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 540
DB 724 GACGGAGAGCTTCAACAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 783
QY 541 GTGAATCTTCAATCTTAAAGCCGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 784 GTGAATCTTCAATCTTAAAGCCGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
QY 601 GACCGGAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 844 GACCGGAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 903
QY 661 TGCCGAGCTTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 904 TGCCGAGCTTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 963
QY 721 AGCTTCCGGAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 964 AGCTTCCGGAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1023
QY 781 TTGAGAGGCGAGAGAGGCGAGCCCGGCGACCCCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB 1024 TTGAGAGGCGAGAGAGGCGAGCCCGGCGACCCCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 1083
QY 841 CACTGTGTGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 1084 CACTGTGTGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1143
QY 901 AAAGAAATGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
DB 1144 AAAGAAATGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1203
QY 961 CAGACGAGCTGTGAGAGAGCAAGAGAGCCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 1204 CAGACGAGCTGTGAGAGAGCAAGAGAGCCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1263
QY 1021 GGCCTGGGCTTGTGACTCAGAGTGTGACCCCGGACCTTGAAGGCGACCTTGTGTGTGTGTGTGT 1080
DB 1264 GGCCTGGGCTTGTGACTCAGAGTGTGACCCCGGACCTTGAAGGCGACCTTGTGTGTGTGTGTGT 1323
QY 1081 CTTGTTTTTGAAGAGCATCAGTCCACCGGACACAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1324 CTTGTTTTTGAAGAGCATCAGTCCACCGGACACAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1383
QY 1141 CGAGAGAGAGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
DB 1384 CGAGAGAGAGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1443
QY 1201 TTCTACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1263
DB 1444 TTCTACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1476
RESULT 12
ADP46448
XX ADP46448 standard; DNA; 1833 BP.
XX
AC ADP46448;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human colon specific nucleic acid SEQ ID NO:24.
XX
KW de; gene; human; colon specific protein; CSP; CSNA; cytosolic; vaccine;
```

KM gene therapy; colon specific nucleic acid; cancer; colon;
KW chromosome 11p15.5.
XX
XX Homo sapiens.
OS
XX WO2004050860-A2.
PN
XX 17-JUN-2004.
PD
XX 04-DEC-2003; 2003WO-US040063.
PF
XX 04-DEC-2002; 2002US-0431132P.
PR 04-DEC-2002; 2002US-0431144P.
XX
XX (DIAD-) DIADEXUS INC.
PA
XX Macina RA, Turner LR, Sun Y;
PI
XX WPI; 2004-480623/45.
DR
XX
XX
PT Novel colon specific protein derived from normal and neoplastic colon
PT cell; useful as vaccine in treating colon cancer and in identifying,
PT diagnosing, monitoring, staging, imaging colon cancer and non-cancerous
PT disease state in colon.
PS
PS Claim 1; SEQ ID NO 24; 547pp; English.
XX
XX The invention relates to a novel colon specific protein (CSP) (I) and the
CC nucleic acid (CSNA) encoding it. A CSP of the invention has cytostatic
CC activity. The protein is useful as a vaccine, and the nucleic acid may
CC have a use in gene therapy. A CSP is useful for determining the presence
CC of a colon specific protein in a sample. A CSNA is useful for determining
CC the presence of a colon specific nucleic acid (CSNA) in a sample. The CSP
CC and CSNA are useful for diagnosing or monitoring the presence and
CC metastases of colon cancer in a patient. A method of the invention is
CC useful for treating a patient with colon cancer. A CSP and CSNA are
CC useful in identifying, diagnosing, monitoring, staging, imaging colon
CC cancer and non-cancerous disease state in colon, and as a vaccine for
CC treating colon cancer and non-cancerous disease states in colon. The
CC present sequence represents a CSNA of the invention.
SQ
SQ Sequence 1833 BP; 330 A; 610 C; 564 G; 329 T; 0 U; 0 Other;
Query Match 93.8%; Score 1156; DB 12; Length 1833;
Best Local Similarity 94.8%; Pred. No. 2.6e-221;
Matches 1233; Conservative 0; Mismatches 0; Indels 67; Gaps 1;
QY 1 ATGCCAGGTGTCTGTGATAGAGGCCCTGACTTCTCTCCCGCTGTGAGACAGAGTGTG 60
Db 353 ATGCCAGGTGTCTGTGATAGAGGCCCTGACTTCTCTCCCGCTGTGAGACAGAGTGTG 412
QY 61 AGGCTTCGCTTGGGCACTAGTGGCTTGAACCTGACCGGCTTGGGTAGTCTTGGGCC 120
Db 413 AGGCTTCGCTTGGGCACTAGTGGCTTGAACCTGACCGGCTTGGGTAGTCTTGGGCC 472
QY 121 CACTGCTCCTGTGCTTCACTGCACTGAGTGAAGACGAGGCTTCATTGGGAATTGGAGG 180
Db 473 CACTGCTCCTGTGCTTCACTGCACTGAGTGAAGACGAGGCTTCATTGGGAATTGGAGG 532
QY 181 CACTAGAGCTTCCACGAGTACTCTGTGGTGAAGGCCAAGCTGTCAAGAGTCTTGTGTC 240
Db 533 CACTAGAGCTTCCACGAGTACTCTGTGGTGAAGGCCAAGCTGTCAAGAGTCTTGTGTC 592
QY 241 AGTGTCTGTGGGGTCAACGTGACCAAGCACTGAAGTCTATGGGGCTTCACTGCTCATC 300
Db 593 AGTGTCTGTGGGGTCAACGTGACCAAGCACTGAAGTCTATGGGGCTTCACTGCTCATC 652
QY 301 CAGAACATCAGCTTCTCCTCTTCACTCTTCAAGAGAGCTGGCCCTCAAGCCAGCTGGCT 360
Db 653 CAGAACATCAGCTTCTCCTCTTCACTCTTCAAGAGAGCTGGCCCTCAAGCCAGCTGGCT 712
QY 361 GCGGTCTGGCTTCCCTCTCTGTGCTTGTGAGCCCTGTGAGCCGCGCTCTTATGTC 420

Db 713 GCGGTCTGGCTTCCCTCTCTGTGCTTGTGAGCCCTGTGAGCCGCGCTCTTATGTC 772
QY 421 AAGTCCCGCTCAAGTGTGTCTGTGATCCAGAGCCGTATGGAGAGTGAATTAAC 480
Db 773 AAGTCCCGCTCAAGTGTGTCTGTGATCCAGAGCCGTATGGAGAGTGAATTAAC 832
QY 481 GACGGGAAGCTTACAGACGCTACGCTTCTCTACAGAGACTGGCCCGAGAGCCGAATTG 540
Db 833 GACGGGAAGCTTACAGACGCTACGCTTCTCTACAGAGACTGGCCCGAGAGCCGAATTG 892
QY 541 GTGAACCTTATCTTAAGCCGCAAGCTGAGCGGCGGTGGGGCTTACAGCTTCTTCTGAC 600
Db 893 GTGAACCTTATCTTAAGCCGCAAGCTGAGCGGCGGTGGGGCTTACAGCTTCTTCTGAC 952
QY 601 GACCGGACCTCTGCGCGGCGGTGAGGCTTCCGCGGACCTCTGGTGAACCTGAGCCG 660
Db 953 GACCGGACCTCTGCGCGGCGGTGAGGCTTCCGCGGACCTCTGGTGAACCTGAGCCG 1012
QY 661 TCCGAGCGCTCATGCTGTGCTTTCGAGAGGCTTCTGAGCCGGGCTGTGTCAGCCAC 720
Db 1013 TCCGAGCGCTCATGCTGTGCTTTCGAGAGGCTTCTGAGCCGGGCTGTGTCAGCCAC 1072
QY 721 AGCTTCC----- 727
Db 1073 AGCTTCCGGGTGGTCCCGCGGCGGTGAGTGGTGGGCCCGACGTAACCCACCCCTGAC 1132
QY 728 -----GGAGAGGCTGTGCGCGGCTGTGAGCTTCAACCGGACCCATCTT 773
Db 1133 GGTCCCGCGCGAGGAGAGGCGCTGTGCGGCTGTGAGCTTCAACCGGACCCATCTT 1192
QY 774 CATCACTTTCGAGGCGCAGAGCGGACCCCGGCAACCGGCGCTTCCGCTGTGCGCA 833
Db 1193 CATCACTTTCGAGGCGCAGAGCGGACCCCGGCAACCGGCGCTTCCGCTGTGCGCA 1252
QY 834 GCAACGCGCACTGTGTAACCTTGTCTGTGAGGCGCGGCTCCGTATCTTCTCCGA 893
Db 1253 GCAACGCGCACTGTGTAACCTTGTCTGTGAGGCGCGGCTCCGTATCTTCTCCGA 1312
QY 894 TTTTGGAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 953
Db 1313 TTTTGGAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1372
QY 954 AGACCCCGCAGACGAGCTGACAGAGCAGACAGACCCCATGCTGATTTCTTGAAGCCGAGT 1013
Db 1373 AGACCCCGCAGACGAGCTGACAGAGCAGACAGACCCCATGCTGATTTCTTGAAGCCGAGT 1432
QY 1014 CCTGAGGGGCCGGGCTTGAAGTCAAGAGTGAACCTGAGAGCGGAGCTTGGGTGT 1073
Db 1433 CCTGAGGGGCCGGGCTTGAAGTCAAGAGTGAACCTGAGAGCGGAGCTTGGGTGT 1492
QY 1074 CCGGGGGCGCTGTTTTGAGAGCATCAGCTCAACCGCAACCAAGTGGGGTCTCGCTGG 1133
Db 1493 CCGGGGGCGCTGTTTTGAGAGCATCAGCTCAACCGCAACCAAGTGGGGTCTCGCTGG 1552
QY 1134 AGAGAGCCGAGACAGGAGGAGTGAAGTCTGAGATCTCGGCTCGGAACTACAGTCCG 1193
Db 1553 AGAGAGCCGAGACAGGAGGAGTGAAGTCTGAGATCTCGGCTCGGAACTACAGTCCG 1612
QY 1194 CACAGACTTCTACTGCTGTGTCTCAAGATGATATGAG 1233
Db 1613 CACAGACTTCTACTGCTGTGTCTCAAGATGATATGAG 1652
RESULT 13
ABK40277
ID ABK40277 standard; cDNA; 1649 BP.
XX
AC ABK40277;
XX
DT 15-JUN-2002 (first entry)
XX
XX cDNA encoding human PR0342 polypeptide.
XX

KM Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukemias; neuronal disorder; stroma disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytoabatic; neuroprotective; gene; ss.
OS Homo sapiens.
XX MO200153486-A1.
XX PD 26-JUL-2001.
XX PF 11-FEB-2000; 2000WO-US003565.
XX PR 08-MAR-1999; 99WO-US005028.
PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145688P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pileri RM, Roy MA, Smith V, Stone DM;
PI Matsubae CK, Wood WI;
XX WPI; 2002-205567/26.
DR P-PSDB; AAU86151.
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX Claim 50; Fig 47; 302pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,
CC breast, etc), leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
CC stromal and blastocoele disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
XX Sequence 1649 BP; 267 A; 554 C; 526 G; 302 T; 0 U; 0 Other;
Query Match 86.9%; Score 1071.8; DB 6; Length 1649;
Best Local Similarity 99.8%; Pred. No. 1.7e-204;
Matches 1073; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCCAGGTGCTGTGATAGGAGCCCTGACTTCTCTCCCGCTGTGAAGACAGAGTCTG 60
DB 104 ATGCCAGGTGCTGTGATAGGAGCCCTGACTTCTCTCCCGCTGTGAAGACAGAGTCTG 163
QY 61 AGGCGTGGCTTGGGACCTGAGTGGCTGTGAAGTGCAGCGGCTGGGAGTCTCTGGGCCC 120
DB 164 AGGCGTGGCTTGGGACCTGAGTGGCTGTGAAGTGCAGCGGCTGGGAGTCTCTGGGCCC 223
QY 121 CACTGCTCCTGCTGCTGAGTGCAGTGGCTGAAGACGGGCTTCATTTGGGAAATTGGGGGC 180
DB 224 CACTGCTCCTGCTGCTGAGTGCAGTGGCTGAAGACGGGCTTCATTTGGGAAATTGGGGGC 283

QY 181 CACTACAGCTTCCACAGAGTACTCTGGGTCAAGGCCAACCTGTGTAGAGAGTCTGTGTCC 240
DB 284 CACTACAGCTTCCACAGAGTACTCTGGGTCAAGGCCAACCTGTGTAGAGAGTCTGTGTCC 343
QY 241 AGTGTCTGGGAGGCAAGTGAACAGAGCACTAAGTCTATGGGGCTTCACTGCTCCATC 300
DB 344 AGTGTCTGGGAGGCAAGTGAACAGAGCACTAAGTCTATGGGGCTTCACTGCTCCATC 403
QY 301 CAGAACATCAGCTTCTCTCTCTTCACTTTTCAGAGAGCTGGCCCTTACAGCCAGCTGGCT 360
DB 404 CAGAACATCAGCTTCTCTCTCTTCACTTTTCAGAGAGCTGGCCCTTACAGCCAGCTGGCT 463
QY 361 GCGGTGCTGGCT 420
DB 464 GCGGTGCTGGCT 523
QY 421 AAGTGCCTGCTCAACGAGTGTGCTCTGGTACAGAGCGGTATGGGAGAGTGAAGTAAC 480
DB 524 AAGTGCCTGCTCAACGAGTGTGCTCTGGTACAGAGCGGTATGGGAGAGTGAAGTAAC 583
QY 481 GACGGAGAGCTTACAGAGCTTACAGTCTCTTACAGAGCTTCCCGAGAGCCGCAAGTTCC 540
DB 584 GACGGAGAGCTTACAGAGCTTACAGTCTCTTACAGAGCTTCCCGAGAGCCGCAAGTTCC 643
QY 541 GTGAATCTTCACTTAAAGCCGACAGTGAAGCGGCTGTGGGCTTCAAGCTTCTCTGGAC 600
DB 644 GTGAATCTTCACTTAAAGCCGACAGTGAAGCGGCTGTGGGCTTCAAGCTTCTCTGGAC 703
QY 601 GACCGGAGAGCTTCCGCGCGGCTGAGAGCCCTCCGCGAGCTTGTGTGAACCTGAGCGGC 660
DB 704 GACCGGAGAGCTTCCGCGCGGCTGAGAGCCCTCCGCGAGCTTGTGTGAACCTGAGCGGC 763
QY 661 TGCCGAGAGCTTCACTGAGTGTGCTTTCGAGAGCTTTCGAGCCGCGCTGTGAGCCAC 720
DB 764 TGCCGAGAGCTTCACTGAGTGTGCTTTCGAGAGCTTTCGAGCCGCGCTGTGAGCCAC 823
QY 721 AGCTTCCGAGAGGAGGCTGTGCTGCGGCTGTGAGTCAACCCGAGAGCCATTTTCATCAC 780
DB 824 AGCTTCCGAGAGGAGGCTGTGCTGCGGCTGTGAGTCAACCCGAGAGCCATTTTCATCAC 883
QY 781 TTGAGAGGAGAGAGGAGGAGAGCCCGGAGCCCGGCGCTGCGGCTGTGAGAGAGAGCCGC 840
DB 884 TTGAGAGGAGAGAGGAGGAGAGCCCGGAGCCCGGCGCTGCGGCTGTGAGAGAGAGCCGC 943
QY 841 CACTGTGTGACTTGTGCTGTGAGAGCCGAGCTCCGTGACTCTTCTCCGATTTTGG 900
DB 944 CACTGTGTGACTTGTGCTGTGAGAGCCGAGCTCCGTGACTCTTCTCCGATTTTGG 1003
QY 901 AAGGAAGTGAAGTGTGCTGCGGAGAGGAGTGTGAGAGCCGAGAGAGAGAGAGCCGC 960
DB 1004 AAGGAAGTGAAGTGTGCTGCGGAGAGGAGTGTGAGAGCCGAGAGAGAGAGAGAGCCGC 1063
QY 961 CAGAGGAGCTGAG 1020
DB 1064 CAGAGGAGCTGAG 1123
QY 1021 GGCAGGAGCTTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
DB 1124 GGCAGGAGCTTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1178
RESULT 14
ADJ37328
ID ADJ37328 standard; cDNA; 1649 BP.
XX
AC ADJ37328;
DT 22-APR-2004 (first entry)
XX
DE Human tumour therapy associated PRO342 cDNA.
XX
KW cytoabatic; gene therapy; PRO; PRO197; PRO207; PRO226; PRO232; PRO243;

XX	PRO255; PRO2629; PRO274; PRO304; PRO339; PRO1558; PRO2779; PRO1185;
KM	PRO1245; PRO31753; PRO57753; PRO7133; PRO7168; PRO5725; PRO202; PRO206;
KM	PRO264; PRO313; PRO342; PRO542; PRO773; PRO861; PRO1216; PRO1686;
KW	PRO1800; PRO3562; PRO9580; PRO539; PRO4316; PRO4980; cancer; tumour;
XX	neoplastic cell growth; neoplastic cell proliferation; carcinoma;
XX	Lymphoma; blastoma; sarcoma; leukaemia; gene; ss.
OS	Homo sapiens.
XX	US2003211096-A1.
PN	
XX	
PD	13-NOV-2003.
XX	
PF	02-AUG-2002; 2002US-00211858.
XX	
PR	31-AUG-1999; 99US-0151689P.
XX	
PR	11-FEB-2000; 2000WO-US003565.
XX	
XX	09-AUG-2001; 2001US-00927796.
XX	
PA	(GETH) GENENTECH INC.
PI	
PI	Ashekzai AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ,
PI	Marsatec SA, Pan U, Pitci RM, Roy MA, Smith V, Stone DM,
PI	Matanabe CK, Wood WI,
XX	
DR	WPI; 2003-901564/82.
XX	
DR	P-PSDB; ADJ37329.
XX	
PT	New isolated PRO polypeptides, useful as targets for the diagnosis,
PT	prevention and treatment of cancers, e.g. lymphoma, blastoma or
PT	leukemia, and as predictors of the prognosis of tumor treatment.
XX	
XX	Claim 50; SEQ ID NO 47; 307p; English.

QY	121	CAC	TGCTCCCTG	CCCTTCA	GTGCTCA	AGTGGCTG	AAAGA	CGGGCTT	CCATT	GGGAAT	TGGGGG	180
Db	224	CAC	TGCTCCCTG	CCCTTCA	GTGCTCA	AGTGGCTG	AAAGA	CGGGCTT	CCATT	GGGAAT	TGGGGG	283
QY	181	CAC	TACAGCTC	CA	CGAGTA	CTCCTGGG	CAAGG	CAACCT	GT	CAGAGG	TGCTGTGTC	240
Db	284	CAC	TACAGCTC	CA	CGAGTA	CTCCTGGG	CAAGG	CAACCT	GT	CAGAGG	TGCTGTGTC	343
QY	241	A	GTGCTGG	GGGGTCA	AGTGA	CCAGCA	CTGAA	GTCTAT	GGGGCTT	CACTG	CTCCATC	300
Db	344	A	GTGCTGG	GGGGTCA	AGTGA	CCAGCA	CTGAA	GTCTAT	GGGGCTT	CACTG	CTCCATC	403
QY	301	CAG	AATAC	AGTTCT	CTCTCTT	CACTCTT	CAAGAGAG	CTGGCCCTA	CAAGCC	ACGGGCT	360	
Db	404	CAG	AATAC	AGTTCT	CTCTCTT	CACTCTT	CAAGAGAG	CTGGCCCTA	CAAGCC	ACGGGCT	463	
QY	361	G	GGGTGCTG	AGCTCC	CTCGTGT	CTGTGCTG	AGCCCTG	ACTG	AGCCCTG	ACTG	ATGTC	420
Db	464	G	GGGTGCTG	AGCTCC	CTCGTGT	CTGTGCTG	AGCCCTG	ACTG	AGCCCTG	ACTG	ATGTC	523
QY	421	A	AGTCCG	CTTCA	AGCTG	CTGCTG	TGTA	CCAGCA	CGCTAT	GGGGAG	TGAGATTAAC	480
Db	524	A	AGTCCG	CTTCA	AGCTG	CTGCTG	TGTA	CCAGCA	CGCTAT	GGGGAG	TGAGATTAAC	583
QY	481	G	ACGGGAA	AGCTTAC	AGACG	CTTAC	AGCTTCTA	CACGAT	CTGCCCCG	AGACCCG	CAATTC	540
Db	584	G	ACGGGAA	AGCTTAC	AGACG	CTTAC	AGCTTCTA	CACGAT	CTGCCCCG	AGACCCG	CAATTC	643
QY	541	G	TGAAC	CTTCAT	CTAAAG	CCGAG	CTGGAG	CGGGCGT	CAAG	CTCTTCT	CTGAGC	600
Db	644	G	TGAAC	CTTCAT	CTAAAG	CCGAG	CTGGAG	CGGGCGT	CAAG	CTCTTCT	CTGAGC	703
QY	601	G	ACCGCG	ACCTC	CTGCG	CGCTG	AGCCCTC	CGCGAC	CTTCT	TGTGTA	ACCTGAC	660
Db	704	G	ACCGCG	ACCTC	CTGCG	CGCTG	AGCCCTC	CGCGAC	CTTCT	TGTGTA	ACCTGAC	763
QY	661	T	GCCGAC	CGCTTAC	TGTGTG	CTTTCCG	ACGCTTCT	CTAGAC	CCGGGCT	GTGTG	CAACAC	720
Db	764	T	GCCGAC	CGCTTAC	TGTGTG	CTTTCCG	ACGCTTCT	CTAGAC	CCGGGCT	GTGTG	CAACAC	823
QY	721	A	GCTTCC	CGGGAA	GGGCTG	AGCCG	CTGAG	CTCAC	CCCGAC	AGACCC	CACTTCT	780
Db	824	A	GCTTCC	CGGGAA	GGGCTG	AGCCG	CTGAG	CTCAC	CCCGAC	AGACCC	CACTTCT	883
QY	781	T	TTCGAG	GGGCA	GAGCG	CGACCC	CGCGCA	CCCGG	CGTCCG	CTGTG	CGCCAG	840
Db	884	T	TTCGAG	GGGCA	GAGCG	CGACCC	CGCGCA	CCCGG	CGTCCG	CTGTG	CGCCAG	943
QY	841	C	ACCTGT	GTGAC	CTTGTG	CTTGTG	AGAGCC	CGGCT	CGGTAC	CTTCTT	CCGATTTT	900
Db	944	C	ACCTGT	GTGAC	CTTGTG	CTTGTG	AGAGCC	CGGCT	CGGTAC	CTTCTT	CCGATTTT	1000
QY	901	A	AAGAAG	GTGAC	GTGCG	CTGCG	GGAA	GTGTG	CGGTAC	CAGG	CCGCTG	960
Db	1004	A	AAGAAG	GTGAC	GTGCG	CTGCG	GGAA	GTGTG	CGGTAC	CAGG	CCGCTG	1060
QY	961	C	AGACG	AGCTG	CA	AGACG	ACCC	CA	TGCTG	ATTTCTT	CGAGCC	1020
Db	1064	C	AGACG	AGCTG	CA	AGACG	ACCC	CA	TGCTG	ATTTCTT	CGAGCC	1120
QY	1021	G	GGCGGG	CCCTG	AGACT	CA	AGGTG	ACCCG	AC	CTT	AGGGCG	1075
Db	1124	G	GGCGGG	CCCTG	AGACT	CA	AGGTG	ACCCG	AC	CTT	AGGGCG	1178

0Y 1 ATGCCAGGAGTGTGTGATGTAGGAGCCCTGACTCTCTCTCCCGTCTGAAGAACAAGGTGTG 60
104 ATGCCAGGAGTGTGTGATGTAGGAGCCCTGACTCTCTCTCCCGTCTGAAGAACAAGGTGTG 163
Db 104 ATGCCAGGAGTGTGTGATGTAGGAGCCCTGACTCTCTCTCCCGTCTGAAGAACAAGGTGTG 163
0Y 61 AGGCTGAGCTTGGGAGAGCTCAATGGGCTTGAATCTGACGACGGCTTGGTATGTCTCTGGGCC 120
Db 164 AGGCTGAGCTTGGGAGAGCTCAATGGGCTTGAATCTGACGACGGCTTGGTATGTCTCTGGGCC 223

RESULT 15	
ADG68252	
ID	ADG68252 standard; cDNA; 1649 BP.
XX	
XX	
AC	ADG68252;
XX	
DT	11-MAR-2004 (first entry)
XX	

DE Human PRO polypeptide cDNA #24.
XX
KM neoplastic tumour; lung; colon; breast; prostate; rectal; cervical;
KM liver; gene therapy; Human; sex; gene.
XX
OS Homo sapiens.
XX
PN US2001170228-A1.
XX
PD 11-SEP-2003.
XX
PF 02-AUG-2002; 2002US-00210951.
XX
PR 31-AUG-1999; 99US-0151689P.
PR 11-FEB-2000; 2000WO-US003565.
PR 09-AUG-2001; 2001US-00927796.
XX
PA (GENTH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan MJ,
PI Marsters SA, Pan J, Plichi RM, Roy MA, Smith V, Stone DM,
PI Matsubara CK, Wood WI;
XX
XX WPI; 2004-020650/02.
DR P-PSDB; ADG68253.
XX
XX
XX New isolated antibodies binding PRO polypeptides, useful for diagnosing,
PT prognosticating and/or treating neoplastic tumors, such as lung, colon,
PT breast, prostate, rectal, cervical and liver tumors.
XX
XX
PS Claim 50; SEQ ID NO 47; 308bp; English.
XX
XX The invention relates to an isolated antibody that binds to a PRO
CC polypeptide. The methods and compositions of the present invention are
CC useful for diagnosing, prognosticating and/or treating neoplastic
CC tumours, such as lung, colon, breast, prostate, rectal, cervical and
CC liver tumours. The PRO polypeptides are also useful as molecular weight
CC markers, or for chromosome identification. The PRO genes are useful as
CC hybridisation probes, or for screening libraries of Human cDNA, genomic
CC DNA or mRNA. The PRO genes may also be used in gene therapy, particularly
CC for replacing a defective gene. The present sequence is used in the
CC exemplification of the invention.
XX
SO Sequence 1649 BP; 267 A; 554 C; 526 G; 302 T; 0 U; 0 Other;
Query Match 86.9%; Score 1071.8; DB 12; Length 1649;
Best Local Similarity 99.8%; Pred. No. 1.7e-204;
Matches 1073; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCCAGGTGCTGTGATAGGAGCCCTGACTTCTCTCCCGTCTGAAGACAGATGCTG 60
DB 104 ATGCCAGGTGCTGTGATAGGAGCCCTGACTTCTCTCCCGTCTGAAGACAGATGCTG 163
QY 61 AGGCGTGGCTTGGGACGCTGAGGCTGTGAACGAGGTTGGTAAAGTCTGGGCCC 120
DB 164 AGGCGTGGCTTGGGACGCTGAGGCTGTGAACGAGGTTGGTAAAGTCTGGGCCC 223
QY 121 CACTGCTCCCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 224 CACTGCTCCCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283
QY 181 CACTACAGCTTCAAGAGTACTCTGAGTCAAGGCAACCTGTGAGAGTGTGTCTC 240
DB 284 CACTACAGCTTCAAGAGTACTCTGAGTCAAGGCAACCTGTGAGAGTGTGTCTC 343
QY 241 AGTGTCTGGGGGTCAAGTGAACGAGCACTGAAGTCTATGGGGCTTCACTGCTCATC 300
DB 344 AGTGTCTGGGGGTCAAGTGAACGAGCACTGAAGTCTATGGGGCTTCACTGCTCATC 403
QY 301 CAGAACATCAGCTTCT 360
DB 404 CAGAACATCAGCTTCT 463

QY 361 GCGGTGCTGGCTCCCTATGTC 420
DB 464 GCGGTGCTGGCTCCCTATGTC 523
QY 421 AAGTGGCTCTCAAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 524 AAGTGGCTCTCAAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
QY 481 GACGGAAGCTCTACAGACGCTTCT 540
DB 584 GACGGAAGCTCTACAGACGCTTCT 643
QY 541 GTGAACCTTCACTTAAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 644 GTGAACCTTCACTTAAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
QY 601 GACCGGACCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 704 GACCGGACCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
QY 661 TGCCGACGCTCATGCTGCTGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTC 720
DB 764 TGCCGACGCTCATGCTGCTGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTC 823
QY 721 AGCTTCCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 824 AGCTTCCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
QY 781 TTGAGGAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 884 TTGAGGAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 943
QY 841 CACTGTGTAACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 944 CACTGTGTAACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003
QY 901 AAAGAAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 1004 AAAGAAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
QY 961 CAGACGAGCTGACAGACGACCAAGACCCCATGCTGATTTCTTTCAGAGGCGAGTCCCTGAG 1020
DB 1064 CAGACGAGCTGACAGACGACCAAGACCCCATGCTGATTTCTTTCAGAGGCGAGTCCCTGAG 1123
QY 1021 GGCCTGGGCTCTGAGCTGAGAGTGAACCCGACCTTGAAGGCGAGCTGAGGTGCTC 1075
DB 1124 GGCCTGGGCTCTGAGCTGAGAGTGAACCCGACCTTGAAGGCGAGCTGAGGTGATGC 1178

Search completed: July 29, 2005, 22:29:56
Job time : 763 secs

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Best Local Similarity 92.5%; Pred. No. 8,4e-165;
Matches 896; Conservative 0; Mismatches 32; Indels 41; Gaps 3;

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QY 148 CTGAAAGACGGGCTTCATTGGGAATGGGGGCACTACAGCTCCACAGATCTCTGG 207
Db 1 CTGAAAGACGGGCTTCATTGGGAATGGGGGCACTACAGCTCCACGAGTCTCTGG 60
QY 208 GTCAAGGACCAACCTGTGAGAGTGTCTGTCCAGTGTCTGGGGGGTCAACGTACAGC 267
Db 61 GTCAAGGACCAACCTGTGAGAGTGTCTGTCCAGTGTCTGGGGGGTCAACGTACAGC 120
QY 268 ACTGAAGTCTATGAGGGGCTTTCACCTGTCTCATTCAGAACTACAGCTTCTCTTCACT 327
Db 121 ACTGAAGTCTATGAGGGGCTTTCACCTGTCTCATTCAGAACTACAGCTTCTCTTCACT 180
QY 328 CTTCAGAGAGTGGCCCTTACAGCCAGAGTGGCGGTGGTGGTCCCTCTGCTCTGG 387
Db 181 CTTCAGAGAGTGGCCCTTACAGCCAGAGTGGCGGTGGTGGTCCCTCTGCTCTGG 240
QY 388 CTGAGCCTGTGCTGGGCGGCTGTCTATGTCAAGTGGCGGTCTCAACGTGCTCTGG 447
Db 241 CTGAGCCTGTGCTGGGCGGCTGTCTATGTCAAGTGGCGGTCTCAACGTGCTCTGG 300
QY 448 TACCAAGACGCGTATGAGGAGGTGAGATAAACGAGGAAAGCTTACGACGCTACGTC 507
Db 301 TACCAAGACGCGTATGAGGAGGTGAGATAAAC----- 333
QY 508 TCCTACAGGACGTCGCCCCGAGACCGGCAATTTGTGTAACCTTCACTTAAAGCCGACGTC 567
Db 334 -----GCGACGTGCCCCGAGACCGGCAATTTGTGTAACCTTCACTTAAAGCCGACGTC 386
QY 568 GAGCGGCGTGGGGGCTTCAAGCTCTTCTGGAAGACCGGACCTCTGCGCGCGCTGAG 627
Db 387 GAGCGGCGTGGGGGCTTCAAGCTCTTCTGGAAGACCGGACCTCTGCGCGCGCGCTGAG 446
QY 628 CCTTCGCGGACCTCTTGTGTAACCTGAGCGCGCTGCGGACGCTCATGTGTCTTTCG 687
Db 447 CCTTCGCGGACCTCTTGTGTAACCTGAGCGCGCTGCGGACGCTCATGTGTCTTTCG 506
QY 688 GAGGCTTCTGTAGCCGGGCTGTGTGAGACCAAGCTTCCGGGAGGGCTGTGCCGGCTG 747
Db 507 GAGGCTTCTGTAGCCGGGCTGTGTGAGACCAAGCTTCCGGGAGGGCTGTGCCGGCTG 566
QY 748 CTGAGAGCTCAACCGGACAGACCATCTTCACTCACTTCAAGAGGACCAAGGCGGACCGCG 807
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QY 808 CACCCGCGCTCGGCTGTGCGGACAGACCGGCACTGTGTACCTTGTCTGTGAGG 867
Db 627 CACCCGCGCTCGGCTGTGCGGACAGACCGGCACTGTGTGACCTTGTCTGTGAGG 686
QY 868 CCGGCGCGGTGACTCTTCTCCGATTTTGGAAAGAGTGGAGCGGCGGCGCGG 927
Db 687 CCGGCGCGGTGACTCTTCTCCGATTTTGGAAAG-AGTGTGAGCTGTGGCGCGG 745
QY 928 AAGGTGGGTACAGGCGGCTGTGAAGAGACCCCGACGAGCTGACAGACCAAGAG 987
Db 746 AAGGTGGGTACAGGCGGCTGTGAAGAGACCCCGACGAGCTGACAGACCAAGAG 805
QY 988 CCAATGTGATTTCTTGAAGCCGAGTCCCTGAAGGGCGGAGCCCTGACCTAGAGTGAAC 1047
Db 806 CCAATGTGATTTCTTGAAGCCGAGTCCCTGAAGGGCGGAGCCCTGAGNACTAGAGTGAAC 865
QY 1048 CCGGAGACCTGAGGGCGGACCTGTGTGTCCGGGGG-----CCTGTTTTTGAAGACCATCA 1101
Db 866 CCGGAGACCTGAGGGCGGACCTGTGTGTCCGGGGGCGGAGGGGCGCGGTTTTTGAAGACCATCA 925
QY 1102 GCTTCACCG 1110
Db 926 GCTTCACCG 934
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RESULT 2

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BI517905
LOCUS      BI517905      763 bp      mRNA      linear      EST 29-AUG-2001
DEFINITION 603041985F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182556 5',
            mRNA sequence.
ACCESSION  BI517905
VERSION    BI517905
KEYWORDS   GI:15342697
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 763)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L1AM1455 row: 1 column: 21
            High quality sequence stop: 739.
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                        /clone="IMAGE:5182556"
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                        /clone_lib="NIH_MGC_116"
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                        pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
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                        female, 71 yo male colon; 46 yo male kidney, and pool of 2
                        stomachs, 62 yo male and 70 yo female. Library is
                        oligo-dT primed and directionally cloned (EcoRV site is
                        destroyed upon cloning). Average insert size 1.4 kb.
                        Insert size range 1-3 kb. Library is normalized and
                        enriched for full-length clones and was constructed by C.
                        Gruber (Invitrogen). Research Genetics tracking code
                        023. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 59.4%; Score 733; DB 4; Length 763;
Best Local Similarity 99.6%; Pred. No. 7,5e-149;
Matches 755; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 272 AAGTCATAGGGGCTTCACTGCTCATCCAGAACATCAAGCTTCTCTTCACTCTTC 331
Db 1 AAGTCATAGGGGCTTCACTGCTCATCCAGAACATCAAGCTTCTCTTCACTCTTC 60
QY 332 AGAGAGCTGAGCCCTACCAAGCAAGTGGCTGCGGTGCTCCCTCTGTGCTCTGG 391
Db 61 AGAGAGCTGAGCCCTACCAAGCAAGTGGCTGCGGTGCTCCCTCTGTGCTCTGG 120
QY 392 CCTGTGCTGGGCGGCTGTCTATGTCAAGTCCGCTTCAACGTGCTGTGTAC 451
Db 121 CCTGTGCTGGGCGGCTGTCTATGTCAAGTCCGCTTCAACGTGCTGTGTAC 180
QY 452 AGGAGCCGATAGGGGAGGTGAGATTAAGAGAGGAAAGCTTACGACGCTACGTCTCT 511
Db 181 AGGAGCCGATAGGGGAGGTGAGATTAAGAGAGGAAAGCTTACGACGCTACGTCTCT 240
QY 512 ACAGGACCTGCCCCGAGGACCGCAAGTTCGTGAATTCCTCAAGCCGACGCTGAGC 571
Db 241 ACAGGACCTGCCCCGAGGACCGCAAGTTCGTGAATTCCTCAAGCCGACGCTGAGC 300
QY 572 GGGGTGGGGCTACAAAGCTTTCCTGAGAGACCGGACCTCTGCGGCGGCTGAGCCCT 631
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Db 301 GGCGTCGGGGGTACAAAGCTCTTCTGAGCAGCCGAGACCTCTGCGCGGCGGTAGGCCCT 360
Qy 632 CCGCGGACCTCTTGTGTGAACCTTGAAGCGGCTGCGGACCGCTCATGTGTGTCTTTCCGACG 691
Db 361 CCGCGGACCTCTTGTGTGAACCTTGAAGCGGCTGCGGACCGCTCATGTGTGTCTTTCCGACG 420
Qy 692 CTTTCTGAGACCGGGGCTGTGTGAGCAGCAAGCTTCCGGGAGGGGCTGTGCGGCTGTGCG 751
Db 421 CTTTCTGAGACCGGGGCTGTGTGAGCAGCAAGCTTCCGGGAGGGGCTGTGCGGCTGTGCG 480
Qy 752 AGCTCACCGGAGACCCATCTTCATCACTTCGAGGGGCAAGGGCGGACCCCGGACCC 811
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Qy 812 CCGGCGCTCCGCTGCTGTGCGGACGACCGGACCTGTGTGACCTTGTGTGTGTGAGGCGCG 871
Db 541 CCGGCGCTCCGCTGCTGTGCGGACGACCGGACCTGTGTGACCTTGTGTGTGTGAGGCGCG 600
Qy 872 GCTCCGAGTCTCTCTCCGATTTTGGAAAGAGTGAAGTGGCGGCTGCGCGGAGG 931
Db 601 GCTCCGAGTCTCTCTCTCCGATTTTGGAAAGAGTGAAGTGGCGGCTGCGCGGAGG 659
Qy 932 TGGGGAACAGGCGGCTGTGAAGAGAGACCCGACGACGCTGTGAGAGACGACGAGACCCCA 991
Db 660 TGGGGAACAGGCGGCTGTGAAGAGAGACCCGACGACGCTGTGAGAGACGAGAGACCCCA 718
Qy 992 TGTGATTTCTTTCAGAGGCGGAGTCCCTGAGGGGCGGGGCC 1029
Db 719 TGTGATTTCTTTCAGAGGCGGAGTCCCTGAGGGGCGGGGCC 756

RESULT 3
LOCUS BG740350 941 bp mRNA linear EST 15-MAY-2001
DEFINITION BG634105F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779337 5',
mRNA sequence.
ACCESSION BG740350
VERSION BG740350.1 GI:14051003
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cga@nci-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM10636 row: 1 column: 02
High quality sequence stop: 856.
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/mol_type="mRNA"
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/clone="IMAGE:4779337"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 58.8%; Score 725.2; DB 4; Length 941;

Best Local Similarity 98.1%; Pred. No. 3.8e-147;
Matches 808; Conservative 0; Mismatches 8; Indels 8; Gaps 7;
Qy 411 GCTCTATGTCAAGTCCGCTCTCAAGCTGTCTCTGTATACAGAGACCGTATGGAGGT 470
Db 1 GCTCTATGTCAAGTCCGCTCTCAAGCTGTCTCTGTATACAGAGACCGTATGGAGGT 60
Qy 471 GAGATTAAGAGCGGGAAGCTTACAGAGCTTACAGAGCTTCTTACAGAGAGTCCCGAGGA 530
Db 61 GAGATTAAGAGCGGGAAGCTTACAGAGCTTACAGAGCTTCTTACAGAGAGTCCCGAGGA 120
Qy 531 CCGCAAGTGTGTGAATCTTCAATCTTAAAGCCGAGCTGAGAGCGGCTGAGGCTCAAGCT 590
Db 121 CCGCAAGTGTGTGAATCTTCAATCTTAAAGCCGAGCTGAGAGCGGCTGAGGCTCAAGCT 180
Qy 591 CTCTCTGAGAGCAGCCGACCTCTGCGCGGCTGAGAGCTTCTGCGGACCTCTTGTGAA 650
Db 181 CTCTCTGAGAGCAGCCGACCTCTGCGCGGCTGAGAGCTTCTGCGGACCTCTTGTGAA 240
Qy 651 CTGAGGCGCTGCGGACCTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTG 710
Db 241 CTGAGGCGCTGCGGACCTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTG 300
Qy 711 GTGAGGACAGAGCTTCTGAGAGGCTGTGCGGCTGCTGAGAGCTCAAGAGCTCAAGCT 770
Db 301 GTGAGGACAGAGCTTCTGAGAGGCTGTGCGGCTGCTGAGAGCTCAAGAGCTCAAGCT 360
Qy 771 CTTCATCATCTTGAAGGCGAGAGGCGGACCCGCGGCTGCGGCTGCGGCTGCGGCTGCGG 830
Db 361 CTTCATCATCTTGAAGGCGAGAGGCGGACCCGCGGCTGCGGCTGCGGCTGCGGCTGCGG 420
Qy 831 CAGACACCGGACCTGCTGTGACCTTGTCTGTGAGAGCCGGGCTCCGTGACTCTTCTCTC 890
Db 421 CAGACACCGGACCTGCTGTGACCTTGTCTGTGAGAGCCGGGCTCCGTGACTCTTCTCTC 480
Qy 891 CGATTTTGGAAAGAGATGTCAGCTGTGCGGCTGCGGAGAGTGTGAGAGGCGGCTGAG 949
Db 481 CGATTTTGGAAAGAGATGTCAGCTGTGCGGCTGCGGAGAGTGTGAGAGGCGGCTGAG 540
Qy 950 AAGAGAGACCCGAGAGCGGAGCTGC-AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1008
Db 541 AAGAGAGACCCGAGAGCGGAGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 1009 CAGATCCTTGAAGGCGGCGGCTGTG-ACTAGAGAGTGAAGAGAGAGAGAGAGAGAG 1067
Db 601 CAGATCCTTGAAGGCGGCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 1068 GGGGTGTCGGGAGGCTGTTTGGAGAGAGCATGATCAAGAGAGAGAGAGAGAGAGAG 1127
Db 661 GGGGTGTCGGGAGGCTGTTTGGAGAGAGCATGATCAAGAGAGAGAGAGAGAGAGAG 720
Qy 1128 GCTGGG-AGAGAGCGGAGAGCA--GCGAAGTGAAGCTTCGAGATCTCGGAGAACTA 1184
Db 721 GCTGGGAGAGAGAGCGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 1185 CAGTGCCTGAGCA-GACTTCTACTGCTT-GGTGTCAAGAGATGA 1226
Db 781 CAGTGCCTGAGCAAGTCTTCTACTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 824

RESULT 4
LOCUS BX400205/c 983 bp mRNA linear EST 28-APR-2004
DEFINITION BX400205 Homo sapiens T CELLS (JURKAT CELL LINE) COR 10-NORMALIZED
Homo sapiens cDNA clone CS0D005E04 3-PRIME, mRNA sequence.
ACCESSION BX400205
VERSION BX400205.2 GI:46847557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 983)

DEFINITION BX369506 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION BX369506
VERSION BX369506.2 GI:46833010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 839)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30457818.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. .839
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D015YD03"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_1ib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 52.0%; Score 640.6; DB 5; Length 839;
Best Local Similarity 99.4%; Pred. No. 9.5e-129;
Matches 643; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
587 AGCTCTTCTGAGACCGGACCTCTGCGGCGCTGAGCCCTCGGACCTCTTG 646
12 AGCTCTTCTGAGACCGGACCTCTGCGGCGCTGAGCCCTCGGACCTCTTG 71
647 TGAACCTGAGCCGCTGCGGACCTCTGAGCTCTTCTGAGCGCTTGAGCG 706
72 TGAACCTGAGCCGCTGCGGACCTCTGAGCTCTTCTGAGCGCTTGAGCG 131
707 CTTGCTGAGCGGACCTCTGCGGAGGCTGTCGCGGCTGCTGAGCTTACCGG 766
132 CTTGCTGAGCGGACCTCTGCGGAGGCTGTCGCGGCTGCTGAGCTTACCGG 191
767 CCATCTTCATCAGCTTCTGAGGCGGACGCGGCGGACCGGCGGCTCGGCTG 826
192 CCATCTTCATCAGCTTCTGAGGCGGACGCGGCGGACCGGCGGCTCGGCTG 251
827 TGGCGGACGACCGGACCTGAGCTTCTGCTGCTGAGACCGGCTCGGCTCT 886
252 TGGCGGACGACCGGACCTGAGCTTCTGCTGCTGAGACCGGCTCGGCTCT 311
887 CTTCCGATTTTGGAGAGAGTGAAGTGGCGCTGCGGAGAGTGGTACAGCGG 946
312 CTTCCGATTTTGGAGAGAGTGAAGTGGCGCTGCGGAGAGTGGTACAGCGG 371
947 TGGAG 1006
372 TGGAG 431
1007 GCCGAGTCCCTGAGGCGGCGGCTTGAGCTCAGAGGTGAGCCCGGACCTTGA 1066

Db 432 GCGAGTCCCTGAGAGGCGGCGGCTGAGCTCAGAGGTGAGCCCGGACCTGAGGCGGAC 491
Qy 1067 TGGGTCTCCGAGGCGGCTGTTTGGAGAGACCTACAGCTCCACCGCACACAGAGGGGTCT 1126
Db 492 TGGGTCTCCGAGGCGGCTGTTTGGAGAGACCTACAGCTCCACCGCACACAGAGGGGTCT 551
Qy 1127 CGCTGAG 1186
Db 552 CGCTGAG 611
Qy 1187 GTGCCGACAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1233
Db 612 GTGCCGACAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 658
RESULT 8
B1821947 749 bp mRNA linear EST 04-OCT-2001
LOCUS 603039758F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180511 5',
DEFINITION mRNA sequence.
ACCESSION B1821947
VERSION B1821947.1 GI:15933497
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 749)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcrabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L1M11450 row: d column: 16
High quality sequence stop: 739.
Location/Qualifiers
1. .749
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5180511"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC library."
ORIGIN
Query Match 51.8%; Score 639.2; DB 4; Length 749;
Best Local Similarity 99.5%; Pred. No. 1.9e-128;
Matches 641; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
203 CTTGGCTCAAGGCGGACCTGTCAGAGAGTCTGTGTCAGTGTCTGAGGGGTCAAGTGA 262
Db 106 CCATGTCAGAGCGGACCTGTCAGAGAGTCTGTGTCAGTGTCTGAGGGGTCAAGTGA 165
Qy 263 CCAGCACTGAAGTCTATGGGGGCTTACCTGCTCCATCCAGAACATCACTTCTCTCT 322
Db 166 CCAGCACTGAAGTCTATGGGGGCTTACCTGCTCCATCCAGAACATCACTTCTCTCT 225

QY 123 TCACTTTGAGAGAGCTGGCCCTTACAAGCCAGTGGCGGTGCTGGCTTCCCTCTG 382
Db 226 TCACTTTGAGAGAGCTGGCCCTTACAAGCCAGTGGCGGTGCTGGCTTCCCTCTG 285
QY 383 TCCGTGCTGGCCCTGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 442
Db 286 TCCGTGCTGGCCCTGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345
QY 443 TCTGCTACCAAGAGCGCTGATGGAGGTGAGATTAACAGACGGAGCTTACGACGCT 502
Db 346 TCTGCTACCAAGAGCGCTGATGGAGGTGAGATTAACAGACGGAGCTTACGACGCT 405
QY 503 ACCGCTCTTACAGAGAGTGGCCCGAGAGACCGCAAGTTCTGTAAGTTCTTAAGCCGC 562
Db 406 ACCGCTCTTACAGAGAGTGGCCCGAGAGACCGCAAGTTCTGTAAGTTCTTAAGCCGC 465
QY 563 AGCTGAGAGCGGCGCTGAGGAGCTTCTGCTGAGAGACCGGAGCTTCTGCGGCGG 622
Db 466 AGCTGAGAGCGGCGCTGAGGAGCTTCTGCTGAGAGACCGGAGCTTCTGCGGCGG 525
QY 623 CTGAGCCCTTCCGCGGAGCTTCTGCTGAGAGCTGAGCGGCTGCGGCTGCTGCTG 682
Db 526 CTGAGCCCTTCCGCGGAGCTTCTGCTGAGAGCTGAGCGGCTGCGGCTGCTGCTG 585
QY 683 TTTCCGAGCGGCTTCTGAGAGCGGCGCTGCTGAGAGCTTCTGCGGAGGCTGCTG 742
Db 586 TTTCCGAGCGGCTTCTGAGAGCGGCGCTGCTGAGAGCTTCTGCGGAGGCTGCTG 645
QY 743 GGGCTGCTGAGAGCTTCTGAGAGCGGCGCTGCTGAGAGCTTCTGCGGAGGCTGCTG 802
Db 646 GGGCTGCTGAGAGCTTCTGAGAGCGGCGCTGCTGAGAGCTTCTGCGGAGGCTGCTG 705
QY 803 CCGCGAGCGGCGGCTTCCGCTGCTGCGGAGAGCGGCGGCTG 846
Db 706 CCGCGAGCGGCGGCTTCCGCTGCTGCGGAGAGCGGCGGCTG 749

RESULT 9 808 bp mRNA linear EST 25-SEP-2001
B1769076 603057053F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5206380 5',
LOCUS mRNA sequence.
DEFINITION
ACCESSION B1769076 GI:15760654
VERSION B1769076
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 808)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: L1AM1517 row: j column: 13
High quality sequence stop: 807.
Location/Qualifiers
1. 808
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5206380"
/lab_host="DH10B"
/clone_11b="NIH_MGC_122"

FEATURES

source

ORIGIN

Query Match 50.0%; Score 616; DB 4; Length 808;
Best Local Similarity 97.4%; Pred. No. 2,1e-123;
Matches 637; Conservative 0; Mismatches 15; Indels 2; Gaps 1;

/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

QY 4 CCAAGTGTCTGTATAGAGGCGCCCTGACTTCTTCCCTGCTGTAAGACAGAGTCTAGG 63
Db 155 CCAAGTGTCTGTATAGAGGCGCCCTGACTTCTTCCCTGCTGTAAGACAGAGTCTAGG 214
QY 64 CTTGCTTGGGAGAGCTTCTGAGTCTGTAAGTGAAGCTTGGTATGCTTGGGCGCCAC 123
Db 215 CTTGCTTGGGAGAGCTTCTGAGTCTGTAAGTGAAGCTTGGTATGCTTGGGCGCCAC 274
QY 124 TGTCTCCCTGCTTCAAGTCAAGTGAAGAGAGGCTTCTGATTTGGGGGCGAC 183
Db 275 TGTCTCCCTGCTTCAAGTCAAGTGAAGAGAGGCTTCTGATTTGGGGGCGAC 334
QY 184 TACAGCTTCCAGAGTACTCTGAGGCTCAAGGCCAACCTGTCAGAGGCTTGTTCAGT 243
Db 335 TACAGCTTCCAGAGTACTCTGAGGCTCAAGGCCAACCTGTCAGAGGCTTGTTCAGT 394
QY 244 GTCCTGGAGGTCAACGTGACAGACAGTGAAGTATGAGGAGCTTCACTGCTCCATCAG 303
Db 395 GTCCTGGAGGTCAACGTGACAGACAGTGAAGTATGAGGAGCTTCACTGCTCCATCAG 454
QY 304 AACATCAGCTTCTTCTTCTTCACTTCAAGAGAGTGGCCCTTCAAGCCAGTGGCTGGC 363
Db 455 AACATCAGCTTCTTCTTCTTCACTTCAAGAGAGTGGCCCTTCAAGCCAGTGGCTGGC 514
QY 364 GTGCTGGAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
Db 515 GTGCTGGAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
QY 424 TGCCTGCTCAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
Db 575 TGCCTGCTCAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
QY 484 GGAAGCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAG 543
Db 635 GGAAGCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAG 694
QY 544 AACCTATCTTAAGAGCGAGCTGAGAGCGGCGCTGAGAGCTTCAAGAGCTTCAAGAG 601
Db 695 AACCTATCTTAAGAGCGAGCTGAGAGCGGCGCTGAGAGCTTCAAGAGCTTCAAGAG 754
QY 602 ACCGAGAGCTTCTGCGGCGCTGAGAGCTTCTGCGGAGAGCTTCTGCTGTAAGCTGA 655
Db 755 ACCGAGAGCTTCTGCGGCGCTGAGAGCTTCTGCGGAGAGCTTCTGCTGTAAGCTGA 808

RESULT 10

CV026019

LOCUS

DEFINITION 621 bp mRNA linear EST 20-AUG-2004
3834 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC003591, mRNA sequence.

ACCESSION CV026019 GI:51483978
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 621)
 AUTHORS Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,
 Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,
 Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,
 Simons, B., Sequeira, R., Boeck, S., Doucette-Scamm, L., Le Peuch, C.,
 Vandenhaute, J., Chisick, M.E., Albaladejo, J.S., Hill, D.E. and Vidal, M.
 TITLE Human ORFeome Version 1.1: a Platform for Reverse Proteomics
 JOURNAL Genome Res. (2004) In press
 COMMENT Contact: Vidal, M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
 results from a PCR reaction using an MGC full-length cDNA as
 template DNA and ORF specific primers
 PCR Primers
 FORWARD: ATGCCAGTGTCTGTGAT
 BACKWARD: TACATATCCTCTGGACACGAG
 Insert length: 621 Std. Error: 36.00
 Plate: 11010 row: 08 column: C
 Seq primer: ACTGGCCGTCTTTCACACGCTGCTGAGGAAAC
 High quality sequence start: 96
 High quality sequence stop: 620
 POLYA-No.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="mixed"
 /clone_lib="Full length cDNA from the Mammalian Gene
 Collection"
 /note="Vector: mixed; The ORFs were PCR amplified from the
 MGC (Mammalian Gene Collection) as of April 2004 and
 cloned by recombinational Gateway cloning into pDONR223
 Donor Vector. Reference: MGC (Mammalian Gene Collection)
 Program Team. Generation and Initial Analysis of more than
 15,000 Full-length Human and Mouse cDNA Sequences. PNAS,
 2002, 99(126), 16899-16903"

ORIGIN
 Query Match 49.9%; Score 615.2; DB 7; Length 621;
 Best Local Similarity 99.4%; Pred. No. 3.1e-123;
 Matches 617; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ATGCCAGTGTCTGTGATAGGAGCCCTGACTTCTCTCCGCTGGAAGCAGTGTCTG 60
 Db 1 ATGCCAGTGTCTGTGATAGGAGCCCTGACTTCTCTCCGCTGGAAGCAGTGTCTG 60
 QY 1 ATGCCAGTGTCTGTGATAGGAGCCCTGACTTCTCTCCGCTGGAAGCAGTGTCTG 60
 Db 1 ATGCCAGTGTCTGTGATAGGAGCCCTGACTTCTCTCCGCTGGAAGCAGTGTCTG 60
 QY 61 AGGCTTGGCTTGGGAGCTCAGTGGCTTGAAGTGGGAGTCTTGGGAGCTTGGGAGCTT 120
 Db 61 AGGCTTGGCTTGGGAGCTCAGTGGCTTGAAGTGGGAGTCTTGGGAGCTTGGGAGCTT 120
 QY 121 CACTGCTCCTGCTTCACTCAGTGGCTGAAGAGCGGCTTCATTGGGAATTTGGGGAGC 180
 Db 121 CACTGCTCCTGCTTCACTCAGTGGCTGAAGAGCGGCTTCATTGGGAATTTGGGGAGC 180
 QY 121 CACTGCTCCTGCTTCACTCAGTGGCTGAAGAGCGGCTTCATTGGGAATTTGGGGAGC 180
 Db 121 CACTGCTCCTGCTTCACTCAGTGGCTGAAGAGCGGCTTCATTGGGAATTTGGGGAGC 180
 QY 181 CACTACAGCTTCCACAGATCTCTGTGGTCAAGGCCAAGCTGTCAAGAGTGTGTGTC 240
 Db 181 CACTACAGCTTCCACAGATCTCTGTGGTCAAGGCCAAGCTGTCAAGAGTGTGTGTC 240
 QY 181 CACTACAGCTTCCACAGATCTCTGTGGTCAAGGCCAAGCTGTCAAGAGTGTGTGTC 240
 Db 181 CACTACAGCTTCCACAGATCTCTGTGGTCAAGGCCAAGCTGTCAAGAGTGTGTGTC 240
 QY 241 AGTGTCTTGGGGGTCAAGTGAAGTCTATGGGGCTTCACTGTCTGCATC 300
 Db 241 AGTGTCTTGGGGGTCAAGTGAAGTCTATGGGGCTTCACTGTCTGCATC 300
 QY 241 AGTGTCTTGGGGGTCAAGTGAAGTCTATGGGGCTTCACTGTCTGCATC 300
 Db 241 AGTGTCTTGGGGGTCAAGTGAAGTCTATGGGGCTTCACTGTCTGCATC 300
 QY 301 CAGAACATCAGCTTCTCTCTCACTTCAAGAGAGCTGGCCCTACAGCAGTGGCT 360
 Db 301 CAGAACATCAGCTTCTCTCTCACTTCAAGAGAGCTGGCCCTACAGCAGTGGCT 360
 QY 301 CAGAACATCAGCTTCTCTCTCACTTCAAGAGAGCTGGCCCTACAGCAGTGGCT 360
 Db 301 CAGAACATCAGCTTCTCTCTCACTTCAAGAGAGCTGGCCCTACAGCAGTGGCT 360
 QY 361 GCGGTCTGGCTTCTCTCTGTGCTGTGAGCCCTGTGCTGTGAGCCGCTCTTATGTC 420
 Db 361 GCGGTCTGGCTTCTCTCTGTGCTGTGAGCCCTGTGCTGTGAGCCGCTCTTATGTC 420

Db 361 GCGGTCTGGCTTCTCTCTGTGCTGTGAGCCCTGTGCTGTGAGCCGCTCTTATGTC 420
 QY 421 AAGTCCCTCTCAAGCTGTGCTTCTGCTACACAGACCGCTATGGAGGTGAGATTAAC 480
 Db 421 AAGTCCCTCTCAAGCTGTGCTTCTGCTACACAGACCGCTATGGAGGTGAGATTAAC 480
 QY 481 GACGGGAAGCTCTACAGACCGCTTCTGCTTCAAGAGACTGCCCCAGAGACCGAAGTTC 540
 Db 481 GACGGGAAGCTCTACAGACCGCTTCTGCTTCAAGAGACTGCCCCAGAGACCGAAGTTC 540
 QY 541 GTGAATCTATCTTAAAGCCGAGCTGAGCGGCGTGGGGCTTCAAGCTTCTTGAGAC 600
 Db 541 GTGAATCTATCTTAAAGCCGAGCTGAGCGGCGTGGGGCTTCAAGCTTCTTGAGAC 600
 QY 601 GACCGGACCTCTGCGCGC 621
 Db 601 GACCGGACCTCTGCGCGC 621

RESULT 11
 B1518182/C
 LOCUS B1518182 791 bp mRNA linear EST 28-AUG-2001
 DEFINITION 603041985T1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182556 3',
 mRNA sequence.
 ACCESSION B1518182
 VERSION B1518182.1 GI:15342974
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 791)
 NIH-MGC <http://img.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL1455 row: 1 column: 21
 High quality sequence start: 40
 High quality sequence stop: 733.
 Location/Qualifiers
 1..791
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5182556"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo female, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5182556"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo female, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 49.2%; Score 606.6; DB 4; Length 791;
 Best Local Similarity 98.0%; Pred. No. 2.3e-121;
 Matches 646; Conservative 0; Mismatches 9; Indels 4; Gaps 3;

FEATURES	LOCATION	QUALITY	SEQUENCE	SCOP	EST
QY	57.9	999	GGGCGCTCAAAAGCCTCTTCGAGACGACCGGACCTCTTCGCGGGGCGTGAAGCCTC	-CGCGC	637
Db	790	GGGCTCAAAAGCCTCTTCGAGACGACCGGACCTCTTCGCGGGGCGTGAAGCCTCTTCGCGC			731
QY	63.8	ACCTCTTGGTGAACCTGAGCCGCTCCCGACGCGCTCATCGTGGTGTCTTTCGAGCGCTTCC			697
Db	730	ACCTCTTGGTGAACCTGAGCCGCTCCCGACGCGCTCATCGTGGTGTCTTTCGAGCGCTTCC			671
QY	69.8	TGAGCCGGGCGCTGGTGCAGACCAACGCTTCCGGGAGGGCGCTGTGCGGCTGTGAGCTCA			757
Db	670	TGAGCCGGGCGCTGGTGCAGACCAACGCTTCCGGGAGGGCGCTGTGCGGCTGTGAGCTCA			611
QY	75.8	CCCGGAGAACCCATCTTTCATCACTTTCGAGGGGCGAAGGCGC-GACCCCGCGACCCGGC			816
Db	610	CCCGGAGAACCCATCTTTCATCACTTTCGAGGGGCGAAGGCGCGTGAACCCCGCGACCCGGC			551
QY	81.7	CTCCGCGCT--GCTGGCGCCAGCACCGCGCACCTGTGTACCTGTGCTGTGAGGGCCGGCT			874
Db	550	CTCCGCGCTGTGCTGGCGCCAGCACCGCGCACCTGTGTACCTGTGCTGTGAGGGCCGGCT			491
QY	87.5	CCGTGACTCTTTCCTCCGATTTTTCGAAAAGAGTGACGTGGCGCTGCGCGGAGGTGC			934
Db	490	CCGTGACTCTTTCCTCCGATTTTTCGAAAAGAGTGACGTGGCGCTGCGCGGAGGTGC			431
QY	93.5	GGTACAGGCGCGGTGGAAGAGACCCCGACAGCCAGCTGACAGAGACAAAGACCCCATGC			994
Db	430	GGTACAGGCGCGGTGGAAGAGACCCCGACAGCCAGCTGACAGAGACAAAGACCCCATGC			371
QY	99.5	TGATTCCTCGAGGCGGAGTCCCTGAGGGGCGGGGCGCTGAGCTCAAGGTGTGACCCGAGAC			105
Db	370	TGATTCCTCGAGGCGGAGTCCCTGAGGGGCGGGGCGCTGAGCTCAAGGTGTGACCCGAGAC			311
QY	105.5	CTGAGGGGCGACCTGTGGGTGTCCGGGGGCGCTGTTTTCGAGAGCCATCAGCTCCACCGCAC			1114
Db	310	CTGAGGGGCGACCTGTGGGTGTCCGGGGGCGCTGTTTTCGAGAGCCATCAGCTCCACCGCAC			251
QY	111.5	CCAGTGGGGGTCTTCGCTGGGAGAGACCGGAGCGACGAAAGTGTGCTTCGAGTCTCGGCT			1174
Db	250	CCAGTGGGGGTCTTCGCTGGGAGAGACCGGAGCGACGAAAGTGTGCTTCGAGTCTCGGCT			191
QY	117.5	CGCGAACTCAAGTCCCGCGCACAGACTTCTACTGCTGTGTCCAAAGATGATATGTAG			1233
Db	190	CGCGAACTCAAGTCCCGCGCACAGACTTCTACTGCTGTGTCCAAAGATGATATGTAG			132
RESULT 12					
LOCUS	BM924346	1106 bp	mRNA	linear	EST 12-MAR-2002
DEFINITION	AGENCOURT_6630582 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760639				
ACCESSION	BM924346				
KEYWORDS	BM924346.1 GI:19374725				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (baaes 1 to 1106)				
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cga@bbs-rcmail.nih.gov				
	Tissue Procurement: Life Technologies, Inc.				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNLN at:				
	http://image.lnl.gov				
	Plate: LLM12807 row: p column: 16				
	High quality sequence scop: 655.				
	Location/Qualifiers				

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source
1. 1106
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5760639"
/lab_host="DH10B"
/clone_11b="N1H_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site, 1: NotI; site, 2: EcoRV (destroyed);
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of
stomach, 62 yo male and 70 yo female. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match      48.8%; Score 601.4; DB 5; Length 1106;
Best Local Similarity 93.2%; Pred. No. 3,2e-120;
Matches 728; Conservative 0; Mismatches 41; Indels 12; Gaps 5

QY      1 ATGCCAGGTGCTGTGTGATNAGGGGCCCTGACTCTCTCTCCCGCTGTGAAGACCAAGTGTCTG 60
DB      198 ATGCCAGGTGCTGTGTGATNAGGGGCCCTGACTCTCTCTCCCGCTGTGAAGACCAAGTGTCTG 25
QY      61 AGGCGTCGCTTGGGCAAGCTCAATGGGTCTGAACTGACCGGCTTGGGTAGTCTCTGGGCC 122
DB      258 AGGCGTCGCTTGGGCAAGCTCAAGTGGGTCTGAACTGACCGGCTTGGGTAGTCTCTGGGCC 317
QY      121 CACTGCTCCCTGCTTCACTCAAGTGGCTGAAAGACGGGCTTCATTGGGAATTGGGGGC 180
DB      318 CACTGCTCCCTGCTTCACTCAAGTGGCTGAAAGACGGGCTTCATTGGGAATTGGGGGC 377
QY      181 CACTACAGCTTCACGAGTAATCTCTGGGTGCAAGGGCCAACCTGTCAAGAGTCTTGTGTC 240
DB      378 CACTACAGCTTCACGAGTAATCTCTGGGTGCAAGGGCCAACCTGTCAAGAGTCTTGTGTC 437
QY      241 AGTGCCCTGGGGGTCAACGTGACACGACTGAAGTATAGGGGCTTCACTGCTCCATC 300
DB      438 AGTGCCCTGGGGGTCAACGTGACACGACTGAAGTATAGGGGCTTCACTGCTCCATC 497
QY      301 CAGAACATCAGGCTTCCCTCCTTCACTCTTCAGAGAGCTGGCCCTCAAGACCACTGTGCT 360
DB      498 CAGAACATCAGGCTTCCCTCCTTCACTCTTCAGAGAGCTGGCCCTCAAGACCACTGTGCT 557
QY      351 GCGAGTGTGAGCCCTCCCTCTGTGCTCTGAGCTGAGCCCTGACTCTATGTC 420
DB      558 GCGAGTGTGAGCCCTCCCTCTGTGCTCTGAGCTGAGCCCTGACTCTATGTC 617
QY      421 AAGTGCCTCTCAAGTGTGCTCTGTGTACACAGA-CGGGTATGGGAGGTGGAATAAA 479
DB      618 AAGTGCCTCTCAAGTGTGCTCTGTGTACACAGAACCGGTATGGGAGGTGGAATAAA 677
QY      480 CGAGCGGGAAGCTCTACGACGCTTACGTCTCTACAGACGACTGGCCCGAGGACCGCAAGTT 539
DB      678 CGAGCGGGAAGCTCTACGACGCTTACGTCTCTCTACAGACGACTGGCCCGAGGACCGCAAGTT 737
QY      540 CGTGAATCTTCATCTTAAGCCCGCAGCTGAGNC-GGGGTGGGAGCTACAA--GCTCTTCT 596
DB      728 CGTGAATCTTCATCTTAAGCCCGCAGCTGAGGCGGGGGGTGGGGGCTACAAAGCTCTTCTCT 797
QY      557 GAGCAACC-GGCACTCTGTGCGCGCGCTGAGCCCTTCGGCGGACCTCTTGTGTC--AACT 653
DB      798 GAGCAACCAGGCGCAACTCTGTGCGCGCGCTGAGCCCTTCGGCGGACCTCTTGTGTC--AACT 857
QY      654 GAGCGGCTGGCGAGCCTCATGCTGTGTC--CTTTCGAGCGCTT--CCTGAGCGGGGCTG 710
DB      858 AAGCGCTGGCGAGCCTCATGCTGTGAGGATTTTTCGAGCGCGCTTTCCTGAGCGGGGCTG 917
QY      711 GT-GGAGCCACA-GCTTCGCGGAGGGGCTGTGCGCGCTGTGAGTCTCACCGCAGACC 768

```

Db 918 GTGGCAGCCAGGCTTCCCGAAGGCGCTGGGCGCGGCTGGCGGAAACTGACCCCG 977
QY 769 A 769
Db 978 A 978

RESULT 13
BE792803 845 bp mRNA linear EST 20-SEP-2000
LOCUS 601584677F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939162 5',
DEFINITION mRNA sequence.
ACCESSION BE792803
VERSION BE792803.1 GI:10214001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 845)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaobs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
plate: LNCM787 row: 1 column: 19
High quality sequence stop: 790.
Location/Qualifiers
1. 845
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3939162"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 47.8%; Score 589.8; DB 2; Length 845;
Best Local Similarity 97.8%; Pred. No. 1,1e-117;
Matches 609; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

QY 1 ATGCCAGGTGTCTGTATAGAGGCCCTGACTCTCTCCCGTCTGAAGACAGAGTCTG 60
Db 166 ATCCACAGTGTCTGTATAGAGGCCCTGACTCTCTCCCGTCTGAAGACAGAGTCTG 225
QY 61 AGGCCGCTTTGGGAGCTCAGTGGCTCAACTGACGGCTTGGGAGTCTCTGGGCC 120
Db 226 AGGCCGCTTTGGGAGCTCAGTGGCTCAACTGACGGCTTGGGAGTCTCTGGGCC 285
QY 121 CACTGCTCCCTGCTTCACTCAGTGGCTGAAGACGGGCTTCATTGGAAATTGGGGC 180
Db 286 CACTGCTCCCTGCTTCACTCAGTGGCTGAAGACGGGCTTCATTGGAAATTGGGGC 345
QY 181 CACTACAGCTTCAAGATCTCTGGGTCAAGGCCAACTGTCAAGAGTCTTGTTC 240
Db 346 CACTACAGCTTCAAGATCTCTGGGTCAAGGCCAACTGTCAAGAGTCTTGTTC 405

QY 241 AAGTCTCTGGGGGTCAACGTGACCAAGCTGAAGTCTATGGGACCTTCACTGCTCCATC 300
Db 406 AGTGTCTTGGGGGTCAACGTGACCAAGCTGAAGTCTATGGGACCTTCACTGCTCCATC 465
QY 301 CAGAACATCAGCTTCTCTCTCTTCACTCTTCAAGAGAGCTGGCCCTTCAAGACCGAGTGGCT 360
Db 466 CAGAACATCAGCTTCTCTCTCTTCACTCTTCAAGAGAGCTGGCCCTTCAAGACCGAGTGGCT 525
QY 361 GCGGTGCTGGCTCTCTCTCTGCTCTGCTGGCCCTTCTGCTGGCCCTTCTCTATGTC 420
Db 526 GCGGTGCTGGCTCTCTCTCTGCTCTGCTGGCCCTTCTGCTGGCCCTTCTCTATGTC 585
QY 421 AAGTCCCTCTCAACGTGCTCTGCTTCAAGAGAGCTTATGGGAGGTGAGATAAAC 480
Db 586 AAGTCCCTCTCAACGTGCTCTGCTTCAAGAGAGCTTATGGGAGGTGAGATAAAC 645
QY 481 GACGGGAACCTTACAGACGCTTACGCTCTTCAAGGACTGCCCGAGGACCGCAAGTTC 540
Db 646 GACGGGAACCTTACAGACGCTTACGCTCTTCAAGGACTGCCCGAGGACCGCAAGTTC 705
QY 541 GTGAACCTTATCTTAAGCCGCAAGCTGAGCGCGCT--CGGGCTTCAAGCTTCTCTG 598
Db 706 GTGAACCTTATCTTAAGCCGCAAGCTGAGCGCGCTTGGGCTTCAAGCTTCTCTG 765
QY 599 ACGACCGGACCTCTGCGCGCGC 621
Db 766 ACGAACGGGACCTCTGCGCGCGC 788

RESULT 14
BX341382 1003 bp mRNA linear EST 07-APR-2004
LOCUS BX341382
DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION BX341382
VERSION BX341382.2 GI:46274994
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1003)
L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30341987.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and EcoR V
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1003
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ015YD03"
/cell_line="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_1lb="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 47.5%; Score 585.4; DB 5; Length 1003;

Best Local Similarity 96.5%; Pred. No. 9.7e-117;
Matches 628; Conservative 3; Mismatches 14; Indels 6; Gaps 3;

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QY 1 ATGCGAGAGTCTGTATAGAGGCCCCGACTCTCTCCCGCTTGAAGACAGAGTCTG 60
DB 300 ATGCGAGAGTCTGTATAGAGGCCCCGACTCTCTCCCGCTTGAAGACAGAGTCTG 359
QY 61 AGGCTCTGCTGGGAGCTGAGTGGCTTGAAGTGAAGAGGCTTGGATAGTCTGGGCCC 120
DB 360 AGGCTCTGCTGGGAGCTGAGTGGCTTGAAGTGAAGAGGCTTGGATAGTCTGGGCCC 419
QY 121 CACTGCTCCCTGCTTCACTCACTGAGTGAAGAGCGGCTTCCATTGGGAATGGGGGC 180
DB 420 CACTGCTCCCTGCTTCACTCACTGAGTGAAGAGCGGCTTCCATTGGGAATGGGGGC 479
QY 181 CACTACAGCTCCACGAGTACTCTGGGTCAAGGCCAAGCTGTGAGAGTGTGTCTC 240
DB 480 CACTACAGCTCCACGAGTACTCTGGGTCAAGGCCAAGCTGTGAGAGTGTGTCTC 539
QY 241 AGTCTCTGGGGGTCACGTCAGACGAGTGAAGTATGGGGGCTTCACTGCTCATC 300
DB 540 AGTCTCTGGGGGTCACGTCAGACGAGTGAAGTATGGGGGCTTCACTGCTCATC 598
QY 301 CAGAACATCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
DB 599 CAGAACATCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 658
QY 361 GCGGTGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 659 GCGGTGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 718
QY 421 AAGTGGCTGTCACGTCGCTCTGTGTACACGACGCTATGGGGAGTGAAGTAAAC 480
DB 719 AAGTGGCTGTCACGTCGCTCTGTGTACACGACGCTATGGGGAGTGAAGTAAAC 778
QY 481 GACGGGAGAGCTCTACGAGCTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 779 GACGGGAGAGCTCTACGAGCTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 838
QY 541 GTGAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
DB 839 GTGAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
QY 601 GACCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 651
DB 898 GACCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 944

```

RESULT 15
BM714596 584 bp mRNA linear EST 28-FEB-2002
LOCUS BM714596
DEFINITION UI-E-EJ0-ahr-n-24-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
ACCESSION UI-E-EJ0-ahr-n-24-0-UI.5', mRNA sequence.
VERSION BM714596
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Bernaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
AUTHORS discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: bento-soares@iowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.research.com).
The following repetitive elements were found in this cDNA
sequence: 35-104, >MER52#unknown (matched complement)
Seq primer: M13 Reverse.

FEATURES

source
Location/Qualifiers
1..584
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-ahr-n-24-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1ib="UI-E-EJ0"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-E-EJ0 is a subcloned cDNA library constructed
according to Bernaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATCAGAG; lens, CGATTAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAGATG; retina, CCGCG;
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 46.6%; Score 575; DB 4; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.7e-114;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 659 GCTGCCGAGCTCTCATCTGCTGCTCTTCCGAGCCCTTCTCTGAGCCGGGCTGTGACGC 718
DB 1 GCTGCCGAGCTCTCATCTGCTGCTCTTCCGAGCCCTTCTCTGAGCCGGGCTGTGACGC 60
QY 719 ACAGCTTCCGGAGAGGCTGTGCTGCTGTGAGCTACCCGAGACCATCTTCACTCA 778
DB 61 ACAGCTTCCGGAGAGGCTGTGCTGCTGTGAGCTACCCGAGACCATCTTCACTCA 120
QY 779 CTTTGAAGGCGAGAGGCGGAGCCCGGCGAGCTCGGCTGTGAGCGGCGAGAC 838
DB 121 CTTTGAAGGCGAGAGGCGGAGCCCGGCGAGCTCGGCTGTGAGCGGCGAGAC 180
QY 839 GCCACCTGTGACCTTGTGCTGTGAGAGCCCGGCTCGGCTGTGAGCTCTCTCCGATTTT 898
DB 181 GCCACCTGTGACCTTGTGCTGTGAGAGCCCGGCTCGGCTGTGAGCTCTCTCCGATTTT 240
QY 899 GGAAGAAGTGCAGCTGCGGCTCCCGGAGAGTGTGAGAGCGGCTGTGAGAGAGAC 958
DB 241 GGAAGAAGTGCAGCTGCGGCTCCCGGAGAGTGTGAGAGCGGCTGTGAGAGAGAC 300
QY 959 CCAGAGCGAGCTGAGAGAGAGCAAGAGACCCCACTGCTTCTTGAAGCGGAGTCCCTG 1018
DB 301 CCAGAGCGAGCTGAGAGAGAGCAAGAGACCCCACTGCTTCTTGAAGCGGAGTCCCTG 360
QY 1019 AGGCGCGGCGCTTGAAGTGAAGAGTGAAGCCCGAGCTTGAAGGCGAGCTGTGTCGG 1078
DB 361 AGGCGCGGCGCTTGAAGTGAAGAGTGAAGCCCGAGCTTGAAGGCGAGCTGTGTCGG 420

QY	1079	GGCCTGTTTTTGAGAGCCATCAGCTCCACCGCACACAGTGGGGTCTCGCTGGAGAGA	1138
Db	421	GGCCTGTTTTTGAGAGCCATCAGCTCCACCGCACACAGTGGGGTCTCGCTGGAGAGA	480
QY	1139	GCCGAGCAGCGAAGTGAAGTCTCGGATCTCGGCTTCGCGAACTACAGTGCCCGCACAG	1198
Db	481	GCCGAGCAGCGAAGTGAAGTCTCGGATCTCGGCTTCGCGAACTACAGTGCCCGCACAG	540
QY	1199	ACTTCTACTGCTGCTGTCCAGAGATGATGTAG	1233
Db	541	ACTTCTACTGCTGCTGTCCAGAGATGATGTAG	575

Search completed: July 30, 2005, 01:21:04
 Job time : 4602 secs

CC study cell-signal transduction and the SIGIRR system, and (d) in gene
CC therapy. Sense and antisense oligonucleotides can be used to inhibit
CC expression of the SIGIRR gene. The proteins of the invention are used:
CC (1) to study cellular processes (immune regulation, proliferation, death,
CC migration, interaction with other cells and inflammation); (11) to
CC identify and purify proteins that associate with SIGIRR ligands and
CC receptors, and to measure their biological activity; (11) in screening
CC for and rational design of, potential inhibitors of activity; (1v)
CC therapeutically against diseases mediated by SIGIRR polypeptide counter-
CC structures; (v) as molecular weight (m.w.) markers in electrophoresis;
CC (vi) for determining isoelectric points of unknown proteins; (vii) as
CC controls for determining the extent of protein fragmentation (e.g. to aid
CC characterization of protein structures by mass spectrometry); (viii) for
CC generation of antibodies (Ab); (ix) to deliver diagnostic or therapeutic
CC agents to cells that express SIGIRR binding molecules

XX Sequence 410 AA;

Query Match 100.0%; Score 2147; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEVCDRAPDPLSPSEDOVLRPALGSSVALNCTAMVVSFGHCLPSVQWKDGLPIGIG 60
DB 1 MPEVCDRAPDPLSPSEDOVLRPALGSSVALNCTAMVVSFGHCLPSVQWKDGLPIGIG 60
QY 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISSFSFTLQRAQPTSHVA 120
DB 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISSFSFTLQRAQPTSHVA 120
QY 121 AVASLILVLLALILALILVYKCRNLVLLWYQDAYGVEINDGKLYDAYVSYSCPEDRKF 180
DB 121 AVASLILVLLALILALILVYKCRNLVLLWYQDAYGVEINDGKLYDAYVSYSCPEDRKF 180
QY 181 VNFILKPOLERRRGYKFLDDBDLPRAPSADILVNLSCRRLLIYVLSDAFLSRACSH 240
DB 181 VNFILKPOLERRRGYKFLDDBDLPRAPSADILVNLSCRRLLIYVLSDAFLSRACSH 240
QY 241 SFEGLCRLELLETRRPIFTFEGORRPAHPALRLRQHRHLVTLMLRGSVTPSSDFW 300
DB 241 SFEGLCRLELLETRRPIFTFEGORRPAHPALRLRQHRHLVTLMLRGSVTPSSDFW 300
QY 301 KEVQALAPRKVYRPVGGPQTOLODDKDPMLILRGVPEGRALDSEVDPDPGDLGVRG 360
DB 301 KEVQALAPRKVYRPVGGPQTOLODDKDPMLILRGVPEGRALDSEVDPDPGDLGVRG 360
QY 361 PVFGEPSAPPHSTGVSIGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410
DB 361 PVFGEPSAPPHSTGVSIGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410

RESULT 2

AAB61139 standard; protein; 410 AA.

AC AAB61139;

DT 30-MAR-2001 (first entry)

DE Human NOV9 protein.

XX Human; NOVX; antiinflammatory; cytostatic; neuroprotective;

KM cerebroprotective; immunomodulator; vulnerary; vasotropic; gene therapy;

KW hyperplasia; tumour; restenosis; psoriasis; Dupuytren's contracture;

XX diabetes; rheumatoid arthritis; cerebral oedema; Alzheimer's disease.

OS Homo sapiens.

XX MO2000075321-A2.

XX 14-DEC-2000.

XX 01-JUN-2000; 2000MO-US015303.

XX 03-JUN-1999; 99US-0137322P.
PR 16-MAR-2000; 2000US-0189810P.
PR 22-MAR-2000; 2000US-0191158P.
PR 30-MAR-2000; 2000US-0193086P.
PR 31-MAY-2000; 2000US-00137322.

XX (CURA-) CURAGEN CORP.

PI Shinkets RA, Fernandes E, Herrman U, Vernet C;

XX MPI; 2001-102403/11.

DR N-PSDB; AAF27857.

PT New NOVX polypeptides and polynucleotides, useful in gene therapy, as a
PT diagnostic marker, protein therapeutic, antibody or small molecule drug
PT target for treating immune, proliferative and metabolic diseases and
PT wound healing.

XX Claim 1; Page 36-38; 194pp; English.

CC The present sequence is a new isolated polypeptide (NOVX). The NOVX
CC polypeptides, NOVX nucleic acids, and anti-NOVX antibodies are useful for
CC treating or preventing NOVX-associated disorders. They are also useful
CC for determining the presence of or a predisposition to a disease
CC associated with altered levels of the NOVX polypeptide or nucleic acid.
CC These NOVX-associated disorders include hyperplasias, tumours,
CC restenosis, psoriasis, Dupuytren's contracture, diabetic complications,
CC rheumatoid arthritis, cerebral lesions, diabetic neuropathies, cerebral
CC oedema, senile dementia or Alzheimer's disease. The NOVX polynucleotides
CC are especially useful in gene therapy. Specifically, NOVX is useful as a
CC diagnostic marker or prognostic marker, protein therapeutic and antibody
CC target or small molecule drug target to treat disorders in the immune
CC response pathway, thyroid and metabolic diseases, bone metabolic
CC disorders, diseases of the pancreas (e.g. diabetes or digestive
CC disorders), proliferative diseases, or tissue regeneration and
CC development (e.g. wound healing or treatment of burns)

XX Sequence 410 AA;

Query Match 100.0%; Score 2147; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEVCDRAPDPLSPSEDOVLRPALGSSVALNCTAMVVSFGHCLPSVQWKDGLPIGIG 60
DB 1 MPEVCDRAPDPLSPSEDOVLRPALGSSVALNCTAMVVSFGHCLPSVQWKDGLPIGIG 60
QY 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISSFSFTLQRAQPTSHVA 120
DB 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISSFSFTLQRAQPTSHVA 120
QY 121 AVASLILVLLALILALILVYKCRNLVLLWYQDAYGVEINDGKLYDAYVSYSCPEDRKF 180
DB 121 AVASLILVLLALILALILVYKCRNLVLLWYQDAYGVEINDGKLYDAYVSYSCPEDRKF 180
QY 181 VNFILKPOLERRRGYKFLDDBDLPRAPSADILVNLSCRRLLIYVLSDAFLSRACSH 240
DB 181 VNFILKPOLERRRGYKFLDDBDLPRAPSADILVNLSCRRLLIYVLSDAFLSRACSH 240
QY 241 SFEGLCRLELLETRRPIFTFEGORRPAHPALRLRQHRHLVTLMLRGSVTPSSDFW 300
DB 241 SFEGLCRLELLETRRPIFTFEGORRPAHPALRLRQHRHLVTLMLRGSVTPSSDFW 300
QY 301 KEVQALAPRKVYRPVGGPQTOLODDKDPMLILRGVPEGRALDSEVDPDPGDLGVRG 360
DB 301 KEVQALAPRKVYRPVGGPQTOLODDKDPMLILRGVPEGRALDSEVDPDPGDLGVRG 360
QY 361 PVFGEPSAPPHSTGVSIGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410
DB 361 PVFGEPSAPPHSTGVSIGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410

RESULT 3	
AB023241	
ID	AB023241 standard; protein; 410 AA.
XX	
XX	AB023241,
AC	
XX	
DT	03-SEP-2003 (first entry)
XX	
DE	Human breast tumour associated protein 47-like polypeptide NOV9.
XX	
KW	Tissue typing; cancer; breast cancer; colon cancer; lung cancer; sarcoma
KW	pancreatic cancer; uterine cancer; organ transplantation disorder;
KW	cardiovascular disease; melanoma; atherosclerosis; diabetes mellitus;
KW	ischemic heart disease; haemorrhage; peripheral vascular disease;
KW	leishmaniasis; hypertension; systemic lupus erythematosus; haematopolesis;
KW	tissue regeneration; wound healing; hyperproliferative disorder;
KW	psoriasis; neural disorder; Parkinson's disease; Alzheimer's disease;
KW	Huntington's disease; multiple sclerosis; amyotrophic lateral sclerosis;
KW	ALS; peripheral neuropathy; nervous system tumour; neurotoxin; tremor;
KW	neuropathy; acute brain injury; peripheral nerve trauma; human; NOVX;
XX	gene therapy; epilepsy; breast tumour associated protein 47.
XX	
OS	Homo sapiens.
XX	
PN	US2003027158-A1.
XX	
PD	06-FEB-2003.
XX	
PF	15-OCT-2001; 2001US-00977418.
XX	
PR	03-JUN-1999; 99US-0137332P.
XX	
PR	16-MAR-2000; 2000US-0189810P.
XX	
PR	22-MAR-2000; 2000US-0191158P.
XX	
PR	30-MAR-2000; 2000US-0193086P.
XX	
PR	03-MAY-2000; 2000US-0201388P.
XX	
PR	31-MAY-2000; 2000US-00584411.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkete RA, Fernandes E, Herrman J, Vernet C;
XX	
XX	WPI, 2003-492028/46.
DR	N-PSDB; ACDA0262.
XX	
PT	New nucleic acid sequence encoding a human breast tumor-associated
PT	protein 47-like polypeptide, useful for treating cardiovascular
PT	disorders, neural disorders, diabetes mellitus and cancers.
XX	
PS	Disclosure; Page 24-25; 100pp; English.
XX	
XX	The invention relates to a new isolated NOV4 nucleic acid. The nucleic
CC	acid is useful for identifying a compound that binds the nucleic acid.
CC	The nucleic acid is useful in gene therapy, in screening assays, in
CC	detection assays e.g. chromosomal mapping, cell and tissue typing and
CC	forensic biology, predictive medicine e.g. diagnostic assays, prognostic
CC	assays, monitoring clinical trials and pharmacogenomics and methods of
CC	treatment including therapeutic and prophylactic. The nucleic acid is
CC	also useful for expressing NOVX protein. The nucleic acid is also useful
CC	to provide polynucleotide reagents e.g. labelled probes that are useful
CC	in an <i>in situ</i> hybridisation technique, for identifying a specific tissue
CC	(for example brain tissue) and for use in forensic science. The nucleic
CC	acid is also useful for mapping genes on a chromosome and thus locating
CC	gene regions associated with genetic disease, identifying an individual
CC	from a minute biological sample and to aid in forensic identification of
CC	biological sample. The nucleic acid is also useful for treating cancer,
CC	especially cancers of the breast, colon, lung, pancreas or uterus, or a
CC	melanoma or sarcoma. The nucleic acid is also useful for treating
CC	disorders related to organ transplantation, cardiovascular diseases,
CC	atherosclerosis, ischemic heart disease, haemorrhage, diabetes mellitus,
CC	peripheral vascular disease, thrombosis, hypertension and systemic lupus
CC	erythematosus. NOVX protein encoded by the nucleic acid is useful for
CC	regulating haemotopoiesis, for regeneration of bone, cartilage, tendon
CC	ligament and/or nerve tissue growth or regeneration and for wound
CC	healing.

16-MAR-2000; 2000US-0189810P.
 PR 22-MAR-2000; 2000US-0191158P.
 PR 30-MAR-2000; 2000US-0193086P.
 PR 03-MAY-2000; 2000US-0201388P.
 PR 31-MAY-2000; 2000US-00584411.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkete RA, Fernandes E, Herrman J, Vernet C;
 DR WPI; 2003-616079/58.
 DR N-PSDB; ADM56382.
 XX
 PT New nucleic acids encoding human cell adhesion molecule-like proteins,
 PT useful for treating e.g. cancers, neurological disorders, viral,
 PT bacterial, fungal, helminthic and protozoal infections.
 PS
 PS Disclosure; SEQ ID NO 18; 78pp; English.

The invention relates to an isolated nucleic acid encoding a human cell adhesion molecule-like protein, comprising a sequence encoding a polypeptide having a sequence appearing as ADM56387, a sequence at least 90% identical to the nucleic acid, a sequence encoding a polypeptide having conservative amino acid substitutions to the protein or a fragment comprising at least 20 nucleotides. Also included are an oligonucleotide sequence that is complementary to (and hybridises under stringent conditions with) the nucleic acid (or a portion of it), a vector comprising the nucleic acid, a cell comprising the vector, a pharmaceutical composition comprising the nucleic acid and a process for identifying a compound that binds the nucleic acid, and a compound identified by the process. Disclosed as new are the cDNA and proteins for novel cell adhesion molecules (termed NOVX, being NOV1-23). The NOVX polypeptide, nucleic acid or antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, ischemic cerebrovascular disease, stroke, Alzheimer's disease or Pick's disease), disorders of vesicular transport (e.g. cystic fibrosis, diabetes mellitus, Grave's disease, or goiter), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune hemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The polypeptides can be used as immunogens to produce antibodies and as vaccines. The sequences may further be used in chromosome mapping, identifying individual from minute biological samples (tissue typing), and in forensic identification of a biological sample. NOTE: The authors have mis-labelled the sequences as they appear on pages 12-28 of the patent, it is clear from table 3, the examples and the claims that the SEQ ID numbers for the cDNAs should be the odd numbers from 1-45 and the proteins should be the even numbers from 2-46. The present sequence represents a NOVX cell adhesion molecule of the invention.

XX
 XX Sequence 410 AA;

Query Match 100.0%; Score 2147; DB 7; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.2e-218;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGVCDBAPDPLSPEDQVLRPALGSSVALNCTAWVYSGHCLPSVQMLKDGILPLGIGG 60
 DB 1 MPGVCDBAPDPLSPEDQVLRPALGSSVALNCTAWVYSGHCLPSVQMLKDGILPLGIGG 60
 QY HYSLHEYSWVKANLSEVLVSSVLGVNTSTEVGAFTCSIONTSFSSFTLQRAQPTSHVA 120
 DB 61 HYSLHEYSWVKANLSEVLVSSVLGVNTSTEVGAFTCSIONTSFSSFTLQRAQPTSHVA 120
 QY 121 AVTASLVLALLLALLLALLLKYKCRNLVLTWQDAYGEVINDGKLYDAYVYSIDCPEDRKF 180
 DB 121 AVTASLVLALLLALLLALLLKYKCRNLVLTWQDAYGEVINDGKLYDAYVYSIDCPEDRKF 180

QY 181 VNFILKPOLERRRGYKFLDDBDRLPRAEPSADLLVNLSCRRLIVLSDAFSLRAMCSH 240
 DB 181 VNFILKPOLERRRGYKFLDDBDRLPRAEPSADLLVNLSCRRLIVLSDAFSLRAMCSH 240
 QY 241 SFREGICRLLELTRRPIFTTFEGQRRDPAPALRLIRQHRHVTLLMRPGSVTPSSDEM 300
 DB 241 SFREGICRLLELTRRPIFTTFEGQRRDPAPALRLIRQHRHVTLLMRPGSVTPSSDEM 300
 QY 301 KEVQALPKPKVYRPPVGGPOTLODDKDPMLILRQVREGRALDSEVPDPPEGDLGVNG 360
 DB 301 KEVQALPKPKVYRPPVGGPOTLODDKDPMLILRQVREGRALDSEVPDPPEGDLGVNG 360
 QY 361 PVFGEPSAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDMM 410
 DB 361 PVFGEPSAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDMM 410

RESULT 5
 ID ADF66745
 AD66745 standard; protein; 410 AA.

AC ADF66745;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Novel human protein NOV9.

KW cytostatic; hepatotropic; vulnary; antipsoptic; osteopathic;
 KW antiarthritic; antiatherosclerotic; haemostatic; vasotropic;
 KW thrombotic; antidiabetic; hypotensive; dermatological;
 KW immunosuppressive; antiinflammatory; immunostimulant; fungicide;
 KW virocid; protozoicide; neuroprotective; antirheumatic; antiarthritic;
 KW antistematic; antiparkinsonian; nootropic; anticonulant;
 KW NOVX modulator; cancer; hypertroliferative disease; cirrhosis; keloid;
 KW psoriasis; tissue hypertrophy; osteoarthritis;
 KW atherosclerotic plaque formation; haemorrhage; ischaemic disease;
 KW thrombosis; diabetes mellitus; hypertension; hypothyroidism;
 KW immune deficiency; severe combined immunodeficiency; SCID; infection;
 KW malaria; candidiasis; autoimmune disorder; connective tissue disease;
 KW multiple sclerosis; systemic lupus; erythemaous; rheumatoid arthritis;
 KW autoimmune pulmonary inflammation; Guillain-Barre syndrome;
 KW autoimmune thyroiditis; insulin dependent diabetes mellitus;
 KW myasthenia gravis; graft-versus-host disease;
 KW autoimmune inflammatory eye disease; asthma; haematopoiesis;
 KW tissue regeneration; wound healing; tissue repair; burn; incision; ulcer;
 KW periodontal disease; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; amyotrophic lateral sclerosis; Shy-Drager syndrome;
 KW human.

OS Homo sapiens.

PN US200319103-A1.

PD 23-OCT-2003.

PF 15-OCT-2001; 2001US-00977639.

PR 03-UTN-1999; 99US-0137322P.
 PR 16-MAR-2000; 2000US-0189810P.
 PR 22-MAR-2000; 2000US-0191158P.
 PR 30-MAR-2000; 2000US-0193086P.
 PR 03-MAY-2000; 2000US-0201388P.
 PR 31-MAY-2000; 2000US-00584411.

PA (CURA-) CURAGEN CORP.

PI Shimkete RA, Fernandes E, Herrman J, Vernet C;

DR WPI; 2004-021196/02.

DR N-PSDB; ADF66744.

PT Novel substantially NOVX polypeptide useful for diagnosing, preventing and treating diseases e.g., cancer, multiple sclerosis, systemic lupus

FT erythematous.
 XX
 PS Disclosure; SEQ ID NO 18; 165pp; English.
 XX
 CC The invention describes a substantially purified polypeptide (I) having
 CC amino acid sequence chosen from a fully defined NOVX sequence (S1) of 708
 CC amino acids as given in the specification, or polypeptide having one or
 CC more conservative amino acid substitutions of (S1), or mutant or variant
 CC of (S1). (I) having (S1) is useful for diagnosing a pathological
 CC condition associated with (I) or its activity in a subject e.g. cancer.
 CC (I) useful in treatment of cancer, hyperproliferative diseases,
 CC chirostis, keloid, psoriasis, tissue hypertrophy, osteoarthritis,
 CC atherosclerotic plaque formation, haemorrhage, ischaemic heart or renal
 CC disease, thrombosis, diabetes mellitus, hypertension, hypothyroidism. (I)
 CC is useful in treatment of various immune deficiencies and disorders such
 CC as severe combined immunodeficiency (SCID), bacterial infection, viral
 CC infection such as herpes viral infection, protozoan infection such as
 CC malaria, fungal infection such as candidiasis. (I) is also useful in
 CC treating autoimmune disorders such as connective tissue disease, multiple
 CC sclerosis, systemic lupus, erythematous, rheumatoid arthritis,
 CC autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune
 CC thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis,
 CC graft-versus-host disease and autoimmune inflammatory eye disease and
 CC asthma. (I) useful in regulation of haematopoiesis, regeneration and
 CC tissue growth of bone, cartilage, tendon, ligament and useful for wound
 CC healing and tissue repair. (I) is also useful in treatment of burns,
 CC infections and ulcers. (I) also useful in treatment of periodontal
 CC disease, Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, and Shy-Drager syndrome. (I) has effective
 CC antitumor and antiinflammatory activity. This is the amino acid sequence
 CC of a novel human NOVX protein.

XX Sequence 410 AA;

Query Match 100.0%; Score 2147; DB 8; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.2e-218;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGVCDRAPDPLSPSEDOVLRPALGSSVALNCTAMVVSCHPCSLPSVQMLKDGILPLGIG 60
 DB 1 MPGVCDRAPDPLSPSEDOVLRPALGSSVALNCTAMVVSCHPCSLPSVQMLKDGILPLGIG 60
 QY HYSLHEYSWKANLSEVLVSGLVNTSTVEGAFCSIONTSFSSFTLORAGPTSHA 120
 DB HYSLHEYSWKANLSEVLVSGLVNTSTVEGAFCSIONTSFSSFTLORAGPTSHA 120
 QY 121 AVLASLVLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLL 180
 DB 121 AVLASLVLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLLALLL 180
 QY 181 VNFILKQLERRRGYKFLDDRDLPPAEPADLLVLSRCRLLIVLSAPFSRANCSH 240
 DB 181 VNFILKQLERRRGYKFLDDRDLPPAEPADLLVLSRCRLLIVLSAPFSRANCSH 240
 QY 241 SPFEGLCRLLELRPIFTFEGGRDPAPRALRLRQHNLVTLMLRGSVTPSSDFW 300
 DB 241 SPFEGLCRLLELRPIFTFEGGRDPAPRALRLRQHNLVTLMLRGSVTPSSDFW 300
 QY 301 KEVQALPRKVRYPVGDPOQOLQDDKPMILRGVPEGRALDSEVDPPEGDLGVRG 360
 DB 301 KEVQALPRKVRYPVGDPOQOLQDDKPMILRGVPEGRALDSEVDPPEGDLGVRG 360
 QY 361 PVGEGPAPRPHGTVSGISGRSSSEVDVSDLSRNYSAATDPYCLVSKDM 410
 DB 361 PVGEGPAPRPHGTVSGISGRSSSEVDVSDLSRNYSAATDPYCLVSKDM 410

RESULT 6
 AD119782
 ID AD119782 standard; protein; 410 AA.
 XX
 AC AD119782;
 XX

DT 22-Apr-2004 (first entry)
 XX
 DE Human NOV9 protein.
 XX
 KW Secreted protein; NOVX; diagnosis; metabolic disorder; diabetes; obesity;
 KW infection; anorexia; cancer; cardiovascular disease; hypertension;
 KW atherosclerosis; neurodegenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; epilepsy; immune disorder; osteoarthritis;
 KW haematopoietic disorder; inflammatory skin disorder; asthma;
 KW dyslipidemia; neurogenesis; cell differentiation; cell proliferation;
 KW haematopoiesis; wound healing; angiogenesis; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomics; gene therapy;
 KW anorectic; cardiac; vitruclide; antibacterial; fungicide; protozoicide;
 KW neurotropic; neuroprotective; dermatological; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 37
 FT Domain /note= "Encoded by NTC"
 FT 138..410
 FT /note = Extracellular domain
 PN US2004002134-A1.
 XX
 PD 01-JAN-2004.
 XX
 XX 15-OCT-2001; 2001US-00977819.
 XX
 PR 03-JUN-1999; 99US-0137322P.
 PR 16-MAR-2000; 2000US-0189810P.
 PR 22-MAR-2000; 2000US-0191158P.
 PR 30-MAR-2000; 2000US-0193086P.
 PR 03-MAY-2000; 2000US-0201388P.
 PR 31-MAY-2000; 2000US-00584411.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Fernandes ER, Herrman JL, Vernet CAM,
 XX
 DR WPI; 2004-070737/07.
 XX
 PT New NOVX nucleic acids encoding human KIAA0768 protein-like and human
 PT protein PRO-228 polypeptides, useful for treating NOVX-associated
 PT disorders.
 XX
 PS Disclosure; SEQ ID NO 18; 95pp; English.
 XX
 CC The present invention is based in part on the discovery of novel secreted
 CC and membrane-bound polypeptides and their encoding polynucleotides. The
 CC nucleic acids and polypeptides are collectively referred as NOVX. The
 CC invention is useful for treating, preventing and diagnosing diseases such
 CC as metabolic disorders, diabetes, obesity, infectious diseases such as
 CC viral, bacterial, fungal, helminthic and protozoal infections, anorexia,
 CC cancer, cardiovascular diseases such as hypertension and atherosclerosis,
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
 CC epilepsy, immune disorders such as osteoarthritis, haematopoietic
 CC disorders, inflammatory skin disorders, asthma and various dyslipidemias.
 CC The invention is also useful as targets for the identification of small
 CC molecules that modulate or inhibit e.g. neurogenesis, cell
 CC differentiation, cell proliferation, haematopoiesis, wound healing and
 CC angiogenesis, as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine and pharmacogenomics. The invention is also
 CC useful in gene therapy. The present sequence is human NOV protein.

QY 1 MPGVCDRAPDPLSPSEDOVLRPALGSSVALNCTAMVVSCHPCSLPSVQMLKDGILPLGIG 60
 Query Match 100.0%; Score 2147; DB 8; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.2e-218;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db 1 MPGVCDRADPFLSPSEDDQVLRPALGSSVALNCTAWVSGPHCSLPBVQMLKQGLPLGIGG 60
Qy 61 HYSLSHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNI SFSSFTLQRA GPTSHVA 120
Db 61 HYSLSHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNI SFSSFTLQRA GPTSHVA 120
Qy 121 AVLASLILVLLALLAALLLVKCRNLVNLWYODAYGVEINIDGKLYDAYVSYSDCPEDRKF 180
Db 121 AVLASLILVLLALLAALLLVKCRNLVNLWYODAYGVEINIDGKLYDAYVSYSDCPEDRKF 180
Qy 181 VNFILKPQLERRRGYKFLDDBDRLPRAPESADLLVNLSCRRLIIVLSDAFISRAMCSH 240
Db 181 VNFILKPQLERRRGYKFLDDBDRLPRAPESADLLVNLSCRRLIIVLSDAFISRAMCSH 240
Qy 241 SFREGICRLLELTRRPIFTTFEGQRDPAPRALRLRQHRLVTLMLMRGSGVTPSSDPW 300
Db 241 SFREGICRLLELTRRPIFTTFEGQRDPAPRALRLRQHRLVTLMLMRGSGVTPSSDPW 300
Qy 301 KEVQALAPRKVRYRPVPGDPQTOLQDDKPMILIRGVPEGRALDSEVDPDPEDLGAVNG 360
Db 301 KEVQALAPRKVRYRPVPGDPQTOLQDDKPMILIRGVPEGRALDSEVDPDPEDLGAVNG 360
Qy 361 PVGGEPSAPPHTSGVSLGESRSSEVDVSDLSGRNYSARTDPFCYLVSKDM 410
Db 361 PVGGEPSAPPHTSGVSLGESRSSEVDVSDLSGRNYSARTDPFCYLVSKDM 410

RESULT 7
AD060255
ID AD060255 standard; protein; 410 AA.
AC AD060255;
XX
DT 15-JUL-2004 (first entry)
DE Human NOV9 protein.
XX
KW Human: NOV9 protein; cancer; hyperproliferative disease; cirrhosis;
keloid; psoriasis; tissue hypertrophy; osteoarthritis;
atherosclerotic plaque formation; haemorrhage; ischaemic heart disease;
renal disease; thrombosis; diabetes mellitus; hypertension;
hypochyroidism; severe combined immunodeficiency; SCID; infection;
malaria; candidiasis; autoimmune disorder; connective tissue disease;
multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
autoimmune pulmonary inflammation; Guillain-Barre syndrome;
autoimmune thyroiditis; myasthenia gravis; graft-versus-host disease;
autoimmune inflammatory eye disease; asthma; burn; incision; ulcer;
periodontal disease; Alzheimer's disease; Parkinson's disease;
Huntington's disease; amyotrophic lateral sclerosis; Shy-Drager syndrome;
haematopoiesis; wound healing; tissue repair; antitumor;
antiinflammatory.
XX
OS Homo sapiens.
XX
PN US200313430-A1.
XX
PD 17-JUL-2003.
XX
PF 15-OCT-2001; 2001US-00977751.
XX
PR 03-JUN-1999; 99US-0137322P.
PR 16-MAR-2000; 2000US-0189810P.
PR 22-MAR-2000; 2000US-0191158P.
PR 30-MAR-2000; 2000US-0193086P.
PR 03-MAY-2000; 2000US-0201388P.
PR 31-MAY-2000; 2000US-00584411.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Fernandes E, Herrman J, Vernet C;
XX
DR WPI; 2004-068928/07.
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DR N-PSDB; AD060254.
XX
PT Novel substantially purified NOV9 polypeptide for treating severe
PT combined immunodeficiency, candidiasis, cancer, asthma, multiple
PT sclerosis, systemic lupus erythematosus.
XX
XX
XX Disclosure; SEQ ID NO 18; 155pp; English.
XX
CC The invention relates to human NOV9 polypeptides and polynucleotides.
CC NOV9 sequences are useful in the treatment of cancer, hyperproliferative
CC diseases, cirrhosis, keloid, psoriasis, tissue hypertrophy,
CC osteoarthritis, atherosclerotic plaque formation, haemorrhage, ischaemic
CC heart or renal disease, thrombosis, diabetes mellitus, hypertension,
CC hypochyroidism, asthma, burns, incisions, ulcers, periodontal disease,
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, Shy-Drager syndrome, immune deficiencies
CC and disorders such as severe combined immunodeficiency (SCID), bacterial
CC infection, viral infection e.g. herpes viral infection, protozoan
CC infection e.g. malaria, fungal infection e.g. candidiasis, autoimmune
CC disorders such as connective tissue disease, multiple sclerosis, systemic
CC lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary
CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin
CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
CC and autoimmune inflammatory eye disease. The invention is useful in
CC regeneration and tissue growth of bone, cartilage, tendon, ligament,
CC haematopoiesis regulation, wound healing and tissue repair. Sequences of
CC the invention also exhibit antitumor and antiinflammatory activities. The
CC present sequence is human NOV9 protein.
XX
SQ Sequence 410 AA;
XX
Query Match 100.0%; Score 2147; DB 8; Length 410;
Best local Similarity 100.0%; Pred. No. 1,2e-218;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPGVCDRADPFLSPSEDDQVLRPALGSSVALNCTAWVSGPHCSLPBVQMLKQGLPLGIGG 60
Db 1 MPGVCDRADPFLSPSEDDQVLRPALGSSVALNCTAWVSGPHCSLPBVQMLKQGLPLGIGG 60
Qy 61 HYSLSHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNI SFSSFTLQRA GPTSHVA 120
Db 61 HYSLSHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNI SFSSFTLQRA GPTSHVA 120
Qy 121 AVLASLILVLLALLAALLLVKCRNLVNLWYODAYGVEINIDGKLYDAYVSYSDCPEDRKF 180
Db 121 AVLASLILVLLALLAALLLVKCRNLVNLWYODAYGVEINIDGKLYDAYVSYSDCPEDRKF 180
Qy 181 VNFILKPQLERRRGYKFLDDBDRLPRAPESADLLVNLSCRRLIIVLSDAFISRAMCSH 240
Db 181 VNFILKPQLERRRGYKFLDDBDRLPRAPESADLLVNLSCRRLIIVLSDAFISRAMCSH 240
Qy 241 SFREGICRLLELTRRPIFTTFEGQRDPAPRALRLRQHRLVTLMLMRGSGVTPSSDPW 300
Db 241 SFREGICRLLELTRRPIFTTFEGQRDPAPRALRLRQHRLVTLMLMRGSGVTPSSDPW 300
Qy 301 KEVQALAPRKVRYRPVPGDPQTOLQDDKPMILIRGVPEGRALDSEVDPDPEDLGAVNG 360
Db 301 KEVQALAPRKVRYRPVPGDPQTOLQDDKPMILIRGVPEGRALDSEVDPDPEDLGAVNG 360
Qy 361 PVGGEPSAPPHTSGVSLGESRSSEVDVSDLSGRNYSARTDPFCYLVSKDM 410
Db 361 PVGGEPSAPPHTSGVSLGESRSSEVDVSDLSGRNYSARTDPFCYLVSKDM 410

RESULT 8
AD020095
ID AD020095 standard; protein; 410 AA.
XX
AC AD020095;
XX
XX
XX 12-AUG-2004 (first entry)
DT
DE Human PRO polypeptide #502.
```

XX Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX
 PN W02004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GENTECH) GENENTECH INC.
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR WPI; 2004-420067/39.
 DR N-PSDB; ADO20094.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7; SEQ ID NO 1004; 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC hemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SQ Sequence 410 AA;
 XX
 Query Match 100.0%; Score 2147; DB 8; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.2e-218;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MPGVCDAPPLFSESDQVLRPALGSSVALNCTMWVSSGPHCSIPSYWMLKDGIPLGIGG 60
 DB 1 MPGVCDAPPLFSESDQVLRPALGSSVALNCTMWVSSGPHCSIPSYWMLKDGIPLGIGG 60
 QY 61 HYSLHEYSWKANLSEVLVSSVGVNTSTEVGAFTCSIONISFSSFTLQRAQPTSHVA 120
 DB 61 HYSLHEYSWKANLSEVLVSSVGVNTSTEVGAFTCSIONISFSSFTLQRAQPTSHVA 120
 QY 121 AVLASLVLALLLALLLYKCRNLVLLMTODAYGEVEINDGKLYDAYVSYSDCPEDRKPF 180
 DB 121 AVLASLVLALLLALLLYKCRNLVLLMTODAYGEVEINDGKLYDAYVSYSDCPEDRKPF 180
 QY 121 AVLASLVLALLLALLLYKCRNLVLLMTODAYGEVEINDGKLYDAYVSYSDCPEDRKPF 180
 DB 121 AVLASLVLALLLALLLYKCRNLVLLMTODAYGEVEINDGKLYDAYVSYSDCPEDRKPF 180
 QY 181 VNFILKPOLERRRGYKFLDDRDLPPAEPADLLVLSRCRRILVLSDAFLSRACSH 240
 DB 181 VNFILKPOLERRRGYKFLDDRDLPPAEPADLLVLSRCRRILVLSDAFLSRACSH 240
 QY 241 SPFEGICRLLELTPRPIFTTEGGRDPAPALRLRLQGHVLTLLMRGSGVTPSSDFW 300
 DB 241 SPFEGICRLLELTPRPIFTTEGGRDPAPALRLRLQGHVLTLLMRGSGVTPSSDFW 300

QY 301 KEVQLAPRKRRYPVGSDPQTQLODDKDPWLLIRGVRPEGRALDSEVDPPEGDLGVRG 360
 DB 301 KEVQLAPRKRRYPVGSDPQTQLODDKDPWLLIRGVRPEGRALDSEVDPPEGDLGVRG 360
 QY 361 PVFEPSPAPHTSGVSLGESRSSVDVSDGSRYSARTDPCVLSKDM 410
 DB 361 PVFEPSPAPHTSGVSLGESRSSVDVSDGSRYSARTDPCVLSKDM 410
 XX
 RESULT 9
 ID ADO19087
 XX ADO19087 standard; protein: 410 AA.
 AC
 XX ADO19087;
 DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #12.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 KW
 OS Homo sapiens.
 XX
 PN W02004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GENTECH) GENENTECH INC.
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR WPI; 2004-420067/39.
 DR N-PSDB; ADO19086.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7; SEQ ID NO 24; 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC hemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SQ Sequence 410 AA;
 XX
 Query Match 100.0%; Score 2147; DB 8; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.2e-218;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVCDRAPDPLSPSEDQVLRPALGSSVALNCTAMVWSGPHCSLPVSOMLKDGLPIGIG 60
DB 1 MGVCDRAPDPLSPSEDQVLRPALGSSVALNCTAMVWSGPHCSLPVSOMLKDGLPIGIG 60
QY 61 HSLHEYSWVKANLSEVLVSIVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHVA 120
DB 61 HSLHEYSWVKANLSEVLVSIVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHVA 120
QY 121 AVLASLVLTLALLALLLVYKCRNLVLLWYQDAYGEVEINDGKLYDAYVYSDCPEDRK 180
DB 121 AVLASLVLTLALLALLLVYKCRNLVLLWYQDAYGEVEINDGKLYDAYVYSDCPEDRK 180
QY 181 VNFILKPOLERRRGYKFLDDBDRLPRAEPSADLVNLSCRRILIVLSDAFLSRACSH 240
DB 181 VNFILKPOLERRRGYKFLDDBDRLPRAEPSADLVNLSCRRILIVLSDAFLSRACSH 240
QY 241 SPREGICRLLELTRRPIFTTFEGQRDPAPALRLRQHRHLVTLLMRGVTTPSSDFW 300
DB 241 SPREGICRLLELTRRPIFTTFEGQRDPAPALRLRQHRHLVTLLMRGVTTPSSDFW 300
QY 301 KEVQALPRKVRYPVEGDPQOTLQDDKPMILIRGRVPEGRLDSEVDPDEGDLGVRG 360
DB 301 KEVQALPRKVRYPVEGDPQOTLQDDKPMILIRGRVPEGRLDSEVDPDEGDLGVRG 360
QY 361 PVGEPSPAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410
DB 361 PVGEPSPAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410

RESULT 10
ADP54078
ID ADP54078 standard; protein; 410 AA.
XX
XX ADP54078;
DT 18-NOV-2004 (first entry)
XX
XX Human PRO protein sequence SEQ ID NO:54.
DE
XX human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antidiabetic; antianemic; antiarthritic;
KW antidiabetic; antidiabetic; antidiabetic; antidiabetic;
KW antidiabetic; antidiabetic; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy.
XX
XX Homo sapiens.
OS
XX MO2004039956-A2.
PN
XX 13-MAY-2004.
PD
XX 28-OCT-2003; 2003MO-US034381.
PF
XX 29-OCT-2002; 2002US-0422472P.
PR
XX (GETH) GENENTECH INC.
PA
XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM,
PI Wood WI, Wu TD;
XX
XX WPI; 2004-376182/35.
DR N-PSDB; ADP54077.
DR
XX New PRO polynucleotides and polypeptides, useful in useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.
XX
PS Claim 1, SEQ ID NO 54; 3009pp; English.
XX
XX The present invention describes an isolated PRO nucleic acid (I). Also

CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianemic, antiarthritic,
CC antidiabetic, antidiabetic, antidiabetic, antidiabetic,
CC antidiabetic, antidiabetic, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.
XX
XX
SO Sequence 410 AA;
Query Match 100.0%; Score 2147; DB 8; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGVCDRAPDPLSPSEDQVLRPALGSSVALNCTAMVWSGPHCSLPVSOMLKDGLPIGIG 60
DB 1 MGVCDRAPDPLSPSEDQVLRPALGSSVALNCTAMVWSGPHCSLPVSOMLKDGLPIGIG 60
QY 61 HSLHEYSWVKANLSEVLVSIVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHVA 120
DB 61 HSLHEYSWVKANLSEVLVSIVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHVA 120
QY 121 AVLASLVLTLALLALLLVYKCRNLVLLWYQDAYGEVEINDGKLYDAYVYSDCPEDRK 180
DB 121 AVLASLVLTLALLALLLVYKCRNLVLLWYQDAYGEVEINDGKLYDAYVYSDCPEDRK 180
QY 181 VNFILKPOLERRRGYKFLDDBDRLPRAEPSADLVNLSCRRILIVLSDAFLSRACSH 240
DB 181 VNFILKPOLERRRGYKFLDDBDRLPRAEPSADLVNLSCRRILIVLSDAFLSRACSH 240
QY 241 SPREGICRLLELTRRPIFTTFEGQRDPAPALRLRQHRHLVTLLMRGVTTPSSDFW 300
DB 241 SPREGICRLLELTRRPIFTTFEGQRDPAPALRLRQHRHLVTLLMRGVTTPSSDFW 300
QY 301 KEVQALPRKVRYPVEGDPQOTLQDDKPMILIRGRVPEGRLDSEVDPDEGDLGVRG 360
DB 301 KEVQALPRKVRYPVEGDPQOTLQDDKPMILIRGRVPEGRLDSEVDPDEGDLGVRG 360
QY 361 PVGEPSPAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410
DB 361 PVGEPSPAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410

RESULT 11
ADP22970
ID ADP22970 standard; protein; 410 AA.
XX
XX ADP22970;
AC
XX 18-NOV-2004 (first entry)
DT
XX
DE PRO polypeptide SEQ ID NO:64.
XX
XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KM osteopathic; antidiabetic; dermatological; antipneumatic; antiallergic;
 KM antineumatic; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS unidentified.
 XX
 PN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GETH) GENENTECH INC.
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX
 DR WPI; 2004-419628/39.
 DR N-PSDB; ADP22969.
 XX
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7, SEQ ID NO 64, 2940pp: English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antipneumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipneumatic, antiallergic,
 CC antineumatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polymyopathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polymyopathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 XX Sequence 410 AA;
 SQ

Query Match 100.0%; Score 2147; DB 8; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.2e-218;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVCDRAPDPLSPSEDOVIRPALGSSVALNCTAMVSGPHCSLPSVQMLKDGJPLGIG 60
 DB 1 MGVCDRAPDPLSPSEDOVIRPALGSSVALNCTAMVSGPHCSLPSVQMLKDGJPLGIG 60
 QY 61 HYSLSHESYWKANLSEVLVSIVGVNTSTEVGAFCSIONISFSSFTLORAGPSHYA 120
 DB 61 HYSLSHESYWKANLSEVLVSIVGVNTSTEVGAFCSIONISFSSFTLORAGPSHYA 120
 QY 121 AVLASLVLALLALALVYKCRNLVLLWYQDAYGEVEINDGKLYDAVYSQCPEDRKF 180
 DB 121 AVLASLVLALLALALVYKCRNLVLLWYQDAYGEVEINDGKLYDAVYSQCPEDRKF 180

QY 181 VNFILKPOLERRRGYKFLDDRDLLPRAEPSADLVNLSRCRLIYVLSAFLSRACSH 240
 DB 181 VNFILKPOLERRRGYKFLDDRDLLPRAEPSADLVNLSRCRLIYVLSAFLSRACSH 240
 QY 241 SFREGCLRLLELTRRPIFTFEGORDDPAHRLRLRQHRLVTLMLMRPGSVTPSSDFW 300
 DB 241 SFREGCLRLLELTRRPIFTFEGORDDPAHRLRLRQHRLVTLMLMRPGSVTPSSDFW 300
 QY 301 KEVQALPARKVRRPVEGDPOTQLQDDKDEMLILRGVPEGRALDSEVDDPEGDLGVRG 360
 DB 301 KEVQALPARKVRRPVEGDPOTQLQDDKDEMLILRGVPEGRALDSEVDDPEGDLGVRG 360
 QY 361 PVGEPSAPPHSTGVSLSGESRSSRVVSDLSGRYRSARTDPCYCLVSKDDM 410
 DB 361 PVGEPSAPPHSTGVSLSGESRSSRVVSDLSGRYRSARTDPCYCLVSKDDM 410

RESULT 12
 AAU86151
 ID AAU86151 standard; protein; 504 AA.
 XX
 AC AAU86151;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human PRO342 polypeptide.
 XX
 KM Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KM leukaemia; neuronal disorder; stromal disorder; blastococcal disorder;
 KM inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
 KM neuroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200153486-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 11-FEB-2000; 2000WO-US003565.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 11-MAR-1999; 99US-0123972P.
 PR 11-MAY-1999; 99US-0133459P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 22-JUN-1999; 99US-0140653P.
 PR 22-JUN-1999; 99US-0140653P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149395P.
 PR 31-AUG-1999; 99US-0151689P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan MJ;
 PI Marsters SA, Pan J, Plichi RM, Roy MA, Smith V, Stone DM;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-205567/26.
 DR N-PSDB; ABK40277.
 XX
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating
 PT benign or malignant tumors, leukemias and lymphoid malignancies,
 PT inflammatory, angiogenic and immunologic disorders.
 XX
 PS Claim 61, Fig 48; 302pp: English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumours (e.g. renal, kidney, bladder,
CC breast, etc), leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastocoeic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC AA086128-AA086162 represent the human PRO polypeptides of the invention
XX
SQ Sequence 504 AA;
Query Match 87.4%; Score 1876; DB 5; Length 504;
Best Local Similarity 96.8%; Pred. No. 1.1e-189;
Matches 360; Conservative 2; Mismatches 2; Indels 8; Gaps 1;
QY 1 MPGVCDRAPDPLSPSEDOVLRLPALGSSVALNCTAMVVGPHCSLPVQWLKDGLPFGIGG 60
DB 1 MPGVCDRAPDPLSPSEDOVLRLPALGSSVALNCTAMVVGPHCSLPVQWLKDGLPFGIGG 60
QY 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISFSFTLQRAQPTSHVA 120
DB 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISFSFTLQRAQPTSHVA 120
QY 121 AVLASLLVLLALLALLVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSNCPEDRKF 180
DB 121 AVLASLLVLLALLALLVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSNCPEDRKF 180
QY 181 VNFILKPOLERRRGYKFLDDBDLPRAPESADLVNLSCRRLIVLSDAFLSRMCSH 240
DB 181 VNFILKPOLERRRGYKFLDDBDLPRAPESADLVNLSCRRLIVLSDAFLSRMCSH 240
QY 241 SFREGICRLLELTRRPIFTFEGQRDPAPRALRLRQHNLVTLMLRGSTVTPSSDFW 300
DB 241 SFREGICRLLELTRRPIFTFEGQRDPAPRALRLRQHNLVTLMLRGSTVTPSSDFW 300
QY 301 KEVQALPRKVRYPVEGDPOTQLODDKPMILKRGVPEGRALDSEVDPDEGDLGM-- 358
DB 301 KEVQALPRKVRYPVEGDPOTQLODDKPMILKRGVPEGRALDSEVDPDEGDLGM-- 358
QY 361 PVEGEPAPRPT 372
DB 361 PVEGEPAPRPT 372
QY 359 -----PAGPHS 364
DB 359 -----PAGPHS 364
RESULT 13
ADJ37329
ID ADJ37329 standard; protein; 504 AA.
XX
AC ADJ37329;
XX
DT 22-APR-2004 (first entry)
XX
DE Human tumour therapy associated PRO342.
XX
KM cytostatic; gene therapy; PRO: PRO197; PRO207; PRO226; PRO232; PRO243;
KM PRO266; PRO269; PRO274; PRO304; PRO339; PRO1558; PRO779; PRO1185;
KM PRO1245; PRO1759; PRO5775; PRO7133; PRO7168; PRO5725; PRO202; PRO206;
KM PRO264; PRO313; PRO342; PRO773; PRO861; PRO1216; PRO1686;
KM PRO1600; PRO3567; PRO850; PRO539; PRO4316; PRO4980; cancer; tumour;
KM neoplastic cell growth; neoplastic cell proliferation; carcinoma;
KM lymphoma; blastoma; sarcoma; leukaemia.
XX
OS Homo sapiens.
XX
PN US2003211096-A1.
XX
PD 13-NOV-2003.
XX
PF 02-AUG-2002; 2002US-00211858.
XX
PR 31-AUG-1999; 99US-0151689P.

PR 11-FEB-2000; 2000WO-US003565.
PR 09-AUG-2001; 2001US-00927796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski P, Gurney AL, Hillan KJ;
PI Marsters SA, Pan Y, Plichi RM, Roy MA, Smith V, Stone DM;
PI Matanabe CK, Wood WJ;
XX
XX WPI, 2003-901564/82.
DR N-PSDB; ADJ37328.
XX
XX New isolated PRO polypeptides, useful as targets for the diagnosis,
PT prevention and treatment of cancers, e.g. lymphoma, blastoma, sarcoma or
PT leukemia, and as predictors of the prognosis of tumor treatment.
PS Claim 61; SEQ ID NO 48; 307pp; English.
XX

CC The invention describes an isolated PRO polypeptide. The PRO polypeptide:
CC has at least 80% amino acid sequence identity to: (1) any one of 35 fully
CC defined sequences of 104-954 amino acids (designated PI-P35) given in the
CC specification, with or without its associated signal peptide; (2) an
CC extracellular domain of any one of the polypeptides of PI-P35, with or
CC without its associated signal peptide; or (3) an amino acid sequence
CC encoded by the full-length coding sequence of the DNA deposited under
CC ATCC accession number 209284, 209358, 209376, 209250, 209508, 209379,
CC 209397, 209786, 209482, 209490, 203312, 55820, 203096, 203155, 203465,
CC PTA-255, PTA-618, PTA-945, PTA-256, 203538, 203661, 203835 or PTA-43; or
CC scores at least 80% positives when compared to any one of the sequences
CC of PI-P35. Specifically claimed are 35 PRO polypeptides, i.e. PRO197, PRO339,
CC PRO207, PRO226, PRO232, PRO243, PRO256, PRO269, PRO274, PRO304, PRO339,
CC PRO1558, PRO779, PRO1185, PRO1245, PRO1759, PRO5775, PRO7133, PRO7168,
CC PRO5225, PRO2027, PRO206, PRO264, PRO313, PRO342, PRO542, PRO773, PRO861,
CC PRO1216, PRO1686, PRO1800, PRO3562, PRO950, PRO539, PRO4316 and PRO4980
CC polypeptides. The PRO polypeptides are useful as targets for the
CC diagnosis, prevention and treatment of cancers, and as predictors of the
CC prognosis of tumor treatment. The nucleic acid molecules, antibodies and
CC antagonists are useful for diagnosing and treating neoplastic cell growth
CC and proliferation, e.g. carcinoma, lymphoma, blastoma, sarcoma or
CC leukemia. The antibodies may be used in screening assays for drug
CC candidates. This is the amino acid sequence of a PRO protein useful in
CC the treatment of cancers.
XX
XX Sequence 504 AA;

Query Match 87.4%; Score 1876; DB 7; Length 504;
Best Local Similarity 96.8%; Pred. No. 1.1e-189;
Matches 360; Conservative 2; Mismatches 2; Indels 8; Gaps 1;
QY 1 MPGVCDRAPDPLSPSEDOVLRLPALGSSVALNCTAMVVGPHCSLPVQWLKDGLPFGIGG 60
DB 1 MPGVCDRAPDPLSPSEDOVLRLPALGSSVALNCTAMVVGPHCSLPVQWLKDGLPFGIGG 60
QY 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISFSFTLQRAQPTSHVA 120
DB 61 HYSLHEYSWKANLSEVLVSGLVNTSTEVYGAFTCSIQNISFSFTLQRAQPTSHVA 120
QY 121 AVLASLLVLLALLALLVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSNCPEDRKF 180
DB 121 AVLASLLVLLALLALLVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSNCPEDRKF 180
QY 181 VNFILKPOLERRRGYKFLDDBDLPRAPESADLVNLSCRRLIVLSDAFLSRMCSH 240
DB 181 VNFILKPOLERRRGYKFLDDBDLPRAPESADLVNLSCRRLIVLSDAFLSRMCSH 240
QY 241 SFREGICRLLELTRRPIFTFEGQRDPAPRALRLRQHNLVTLMLRGSTVTPSSDFW 300
DB 241 SFREGICRLLELTRRPIFTFEGQRDPAPRALRLRQHNLVTLMLRGSTVTPSSDFW 300
QY 301 KEVQALPRKVRYPVEGDPOTQLODDKPMILKRGVPEGRALDSEVDPDEGDLGM-- 358
DB 301 KEVQALPRKVRYPVEGDPOTQLODDKPMILKRGVPEGRALDSEVDPDEGDLGM-- 358

PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226688P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
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 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234977P.
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 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
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 PR 02-OCT-2000; 2000US-0236802P.
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 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
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 PR 20-OCT-2000; 2000US-0241211P.
 PR 20-OCT-2000; 2000US-0241785P.
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 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
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 PR 08-NOV-2000; 2000US-0246476P.
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 PR 08-NOV-2000; 2000US-0246478P.
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 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256179P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251858P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465460/50.
 XX N-PSDB; AAS27325.
 DR
 XX Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders.
 XX
 PS Claim 1; SEQ ID NO 973; 880bp; English.
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative disorders
 CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
 CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
 CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
 CC respiratory disorders, dermatological disorders, in wound healing,
 CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
 CC disease), reproductive system disorders, gastrointestinal disorders
 CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
 CC B-cell responsiveness to pathogens, activators of T-cells, to induce
 CC higher affinity antibodies, and as a means to induce tumour proliferation
 CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17053-
 CC AAU17683 represent novel signal transduction pathway protein, amino acid
 CC sequences of the invention

XX

Query Match 82.0%; Score 1761; DB 4; Length 407;

Best Local Similarity 100.0%; Pred. No. 1.3e-177; Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	70	VKANLSEVLSSVVGNNVTSTEVYGAFTCSIQNI	SPSSFTLQRA	GPTSHVA	AVLASL	LYL	129
Db	67	VKANLSEVLSSVVGNNVTSTEVYGAFTCSIQNI	SPSSFTLQRA	GPTSHVA	AVLASL	LYL	126
Qy	130	LALLLALLLVKCRNLNLLWYQDAYGEVEINDG	KLYDAVYS	SDCPEDRK	FVNFIL	KPOL	189
Db	127	LALLLALLLVKCRNLNLLWYQDAYGEVEINDG	KLYDAVYS	SDCPEDRK	FVNFIL	KPOL	186
Qy	190	ERRRGYKLFDDRDLLPRAEPSADLLVNL	SRCLIVLSDA	FLSRAM	CSHSFREG	CRL	249
Db	187	ERRRGYKLFDDRDLLPRAEPSADLLVNL	SRCLIVLSDA	FLSRAM	CSHSFREG	CRL	246
Qy	250	LELTRRPIPTTPEGORRDPAPALRLROHRH	VTLLMR	PGSVTPSS	DFWKEV	QALPR	309
Db	247	LELTRRPIPTTPEGORRDPAPALRLROHRH	VTLLMR	PGSVTPSS	DFWKEV	QALPR	306
Qy	310	KVRYPVEGDPQTQLQDDKDPMLILRG	VEGRALDSE	VPDPPEG	DGVGR	PVGPSPAP	369
Db	307	KVRYPVEGDPQTQLQDDKDPMLILRG	VEGRALDSE	VPDPPEG	DGVGR	PVGPSPAP	366
Qy	370	PHTSGVSLGESRSSEVDVSDIGSRNYSART	DFYCLV	SKDM			410
Db	367	PHTSGVSLGESRSSEVDVSDIGSRNYSART	DFYCLV	SKDM			407

Search completed: August 1, 2005, 13:53:00
Job time : 168 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2005, 13:34:31 ; Search time 41 Seconds

(without alignments)
962.168 Million cell updates/sec

Title: US-09-598-443-2

Perfect score: 2147
Sequence: 1 MPGVCDRAPFLSPSEBDQVL.....GSRVYSARTDEYCLVSKDMD 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215.5	10.0	570	2 A57535	interleukin 1 recep
2	209.5	9.8	569	2 A36187	interleukin-1 rece
3	204	9.5	562	2 G02426	interleukin-1 rece
4	190.5	8.9	576	2 A32604	interleukin-1 rece
5	189.5	8.8	567	2 S29498	lymphocyte antigen
6	184	8.6	555	2 J01526	interleukin-1 rece
7	176	8.2	1097	2 A29943	toll protein precu
8	168.5	7.8	590	2 I56526	interleukin 1 rece
9	163	7.6	247	2 S42633	Pit-1M protein - r
10	144.5	6.7	1385	2 T13887	tlr protein - fru
11	139.5	6.5	1389	2 T13852	gene wheeler prote
12	128.5	6.0	168	2 I51903	type I interleukin
13	123	5.7	799	2 S18209	fibroblast growth
14	115	5.4	243	2 S11226	MyD88 protein - mo
15	114.5	5.3	786	2 T08664	Toll protein-like
16	113.5	5.3	1323	2 PNO568	connectin 3B - chi
17	111	5.2	26926	1 I38344	ctlin, cardiac mus
18	109.5	5.1	822	2 S19947	fibroblast growth
19	109.5	5.1	822	2 B49150	fibroblast growth
20	103	4.8	650	1 J01450	fibroblast growth
21	102.5	4.8	818	2 J04058	fibroblast growth
22	100.5	4.7	629	2 E70589	protoporphyrin IX
23	99	4.6	379	2 G96754	hypothetical prote
24	98	4.6	363	2 B96754	similar to part of
25	97	4.5	176	2 B96754	similar to downy m
26	96.5	4.5	829	2 J04583	fibroblast growth
27	96.5	4.5	829	2 C96754	similar to part of
28	96.5	4.5	802	1 TVHUP4	fibroblast growth
29	95	4.4	815	2 T41490	hypothetical prote

30	94.5	4.4	411	2 T35102	probable transmemb
31	94.5	4.4	1024	2 G71434	probable limonene
32	94	4.4	365	2 J0780	coxsackie- and ade
33	94	4.4	1896	2 T08851	Down syndrome cell
34	93.5	4.4	275	2 D96754	Similar to part of
35	93.5	4.4	1179	2 T04584	TWV resistance pro
36	93.5	4.4	1344	2 T14316	rig-1 protein - mo
37	93.5	4.4	7962	2 I38346	elastic ctlin - hu
38	93	4.3	764	2 A49448	irregular chiasm C
39	92.5	4.3	371	2 F96754	Similar to ML27 [1
40	92.5	4.3	2783	2 T34416	hypothetical prote
41	92	4.3	871	1 I48696	protein-tyrosine k
42	92	4.3	881	1 I48697	protein-tyrosine k
43	92	4.3	1694	2 S50065	sialoadhesin - mou
44	92	4.3	2149	2 C96695	ribulose biphosph
45	91.5	4.3	357	1 TVHUP2	transforming prote

ALIGNMENTS

RESULT 1

A57535 interleukin 1 receptor accessory protein precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C:Accession: A57535

R:Greenfeder, S.A.; Nunes, P.; Kwee, L.; Labow, M.; Chizzonite, R.A.; Ju, G.

J. Biol. Chem. 270, 13757-13765, 1995

A:Title: Molecular cloning and characterization of a second subunit of the interleukin 1

A:Reference number: A57535, MUID:55293970; PMID:7775431

A:Accession: A57535

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-570 <GRB>

A:Cross-references: UNIPROT:Q61730; GB:X65999; NID:g887520; PIDN:CA59991.1; PID:g88752

C:Superfamily: interleukin-1 receptor type I

C:Keywords: transmembrane protein

Query Match 10.0%; Score 215.5; DB 2; Length 570;
Best Local Similarity 25.6%; Pred. No. 4.9e-10;
Matches 85; Conservative 61; Mismatches 153; Indels 33; Gaps 10;

Qy	9	PDFLSPSEDOYLPRALSSVALNCTAW--VSGPHCSLPVQWLKDG-LPLGIGHYSLH 65
Db	243	PQYSPMDRVYKEKEPEBELVDPCKYVFSTIMSH--NEWMTIDKKDPDVTVDITIN 299
Qy	66	EYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSION----ISFSFTLQAGP---TSH 118
Db	300	ESVSYSTEDETRTQIISIKKVTPEDIRNVYCHARTKGEAEQAARVKKVLPPTYVE 359
Qy	119	VAAVLASLVLALLLALLLVKCRNLVNLVLYOYAGEVE-INDGKLYDAVSYSDPED 177
Db	360	LACGFGATVPLVVLVLI--VYHYVLEWLVLFYRAHFTDITIDGKYDIYVSARVVE 417
Qy	178	RKFVNFILKPQLERRRGYKFLDDRDLPPAEBADILVLSRCRLIVLSDAFISRAW 237
Db	418	EEFVLTLRGVLENEFYGKLCIFRDSLPGLVYDETLSFIQSRRLVVLSPVY---- 473
Qy	238	CHSIFREGCLRLLELTRPIFIIFEG-----QRDPAPRALRLRQHNLVTLMLR- 289
Db	474	----LQGTALDELKAGLENNMGRGINVILVQYKAVKQMKVKELRRAVTVLVIKWG 528
Qy	290	PGSVTPSSDPFKKEVQLAPRKVRYRPEVGGPQ 321
Db	529	EKSKYPPGRFWKQLQVAMPYKSPRMSNDKQ 560

RESULT 2

A36187 interleukin-1 receptor type I precursor - human

C:Species: Homo sapiens (man)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004

QY 213 DLVNLSCRLIVLSDAFLSRWCSHSPREGICRLLE-LTRRPFI---TFEGQRDP 268
 DB 1091 QLVGAPASAKIILVLTNRLATEWNRIFRNAPFHESLRGLAQVLIIETSVSAEADV 1150
 QY 269 AH-----PALRLRQHRLVLTLLMRPGSVTPSSDFWKEVOLALPRKV--RYRVEG 318
 DB 1151 AELSPYKSVFSNRLTLCDRY-----FWEKRYALPIELSPGNNYTL 1193
 QY 319 DPQTQLDDXDKPMLILRGVP 339
 DB 1194 DHHRFKQVPSPGMIFRQAPP 1214

RESULT 11

gene wheeler protein - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T13852
 R/Eldon, B.; Kooyer, S.; D'aveylyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Belien, H.
 Development 120, 885-899, 1994
 A/Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simild
 A/Reference number: 217796; PMID:95324375; PMID:7600965
 A/Accession: T13852
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1389 <ELD>
 A/Cross-references: UNIPROT:Q24591; EMBL:L231171; NID:9415682; PID:91019104; PIDN:AAA792C
 C/Genetic:
 A/Genes: wheeler
 A/Cross-references: FlyBase:FBgn0004364

Query Match 6.5%; Score 139.5; DB 2; Length 1389;
 Best Local Similarity 23.2%; Pred. No. 0.0036;
 Matches 66; Conservative 51; Mismatches 105; Indels 63; Gaps 12;

QY 75 SEVLVSSVLGVNTSTEVGAFVCSIGNISFSSFTLORAGPTSHVAALASLVLLALL 134
 DB 973 SDLLDASASNIS-SSODLAGAIGC-----PCWPAVLVTLFLV 1009
 QY 135 AALLVYKRLNVLVMDAYG---EVEIND-GKLYDAYVSYSDCEDRKFVNFILKPOL 169
 DB 1010 VLIIVFRRSSVMKLFPAHVGRCERFEDACKLYAIIILHS--KDYFVCNIIAEL 1067
 QY 190 ER-RRGYKFLDDRDLPRAPESADLLVNSRCRLIVLSDAFLSRWCSHSPREGICR 248
 DB 1068 EHGRPPRLCTIQORDLPQAS-HLQVVGARASRKILVLTNRLATEWNRIFRNAPFHE 1126
 QY 249 LLE-LTRRPFI---TFEGQRDPAH-----PALRLRQHRLVLTLLMRPGSVTPS 236
 DB 1127 SLRLGLAQVLIETSVSAEADVLESLPYKSVFSNRLTLCDRY----- 1171
 QY 297 SDFWKEVOLALPRKV--RYRVEGDPQTQLDDXDKPMLILRGVP 339
 DB 1172 --FWEKRYALPIELSPGNNYTLDHHRFKQVPSPGMIFRQAPP 1214

RESULT 12

type 1 interleukin-1 receptor - rat (fragment)
 C/Species: Rattus sp. (rat)
 C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 13-Sep-1998
 C/Accession: I51903
 R/Sutherland, D.B.; Varilek, G.W.; Neil, G.A.
 Am. J. Physiol. 266, C1198-C1203, 1994
 A/Title: Identification and characterization of the rat intestinal epithelial cell (IEC-
 A/Accession: I51903
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-169 <RES>
 A/Cross-references: GB:870238; NID:9546976

A:Experimental source: intestinal epithelial IEC-18 cells
 C:Superfamily: interleukin-1 receptor type 1
 C/Keywords: cytokine receptor

Query Match 6.0%; Score 128.5; DB 2; Length 169;
 Best Local Similarity 28.1%; Pred. No. 0.0021;
 Matches 50; Conservative 29; Mismatches 76; Indels 23; Gaps 6;

QY 145 NLLVMDAYGEV--EINDKLYDAYVSYSDCEDRKFV--NFILK--PO-LERRGY 195
 DB 1 DIVLWYRDSGSDFLPPKASDGYADAVLYPKTYGESSFAVLDTFVFKLPEVLEGGFGY 60
 QY 196 KLPLDRDRLPRAPESADLLVNSRCRLIVLSDAFLSRWCSHSPREGICRLLELTR 255
 DB 61 KLPLCGRDYVGEDETLEVTNENVRSHLLIILVRMGSSFCGQSSSEBOAIYDALIRE 120
 QY 256 PIFITF---EGQRDPAHPALRLRQHRLVLTLLMRPGSVTPSSDFWKEVOLALPR 309
 DB 121 GIKIILLELEIDYEMPSIQFIQ-----KHGALCWSGDFKRPQSAKTR 168

RESULT 13

S18209
 fibroblast growth factor receptor 4 precursor (clone 61) - mouse
 N/Alternate names: tyrosine kinase Mbk-11
 N/contains: protein-tyrosine kinase (EC 2.7.1.112)
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C/Accession: S18209; S26751; S30497
 R/Stark, K.L.; McMahon, J.A.; McMahon, A.P.
 Development 113, 641-651, 1991
 A/Title: FGFR-4, a new member of the fibroblast growth factor receptor family, expresse

A/Reference number: S18209; PMID:92146274; PMID:11723680
 A/Accession: S18209
 A/Molecule type: mRNA
 A/Residues: 1-799 <STAL>
 A/Cross-references: UNIPROT:Q03142; EMBL:X59927
 R/Stark, K.L.
 submitted to the EMBL Data Library, May 1991
 A/Reference number: S26751
 A/Accession: S26751
 A/Molecule type: mRNA
 A/Residues: 1-485, 'OVYRAARG', 486-799 <SNR2>
 A/Cross-references: EMBL:X59927; NID:950968; PIDN:CAA42551.1; PID:950969
 R/Gilardi-Hebensreidt, P.; Nleto, M.; Frain, M.; Mattei, M.G.; Chestier, A.; Wilkinson
 Oncogene 7, 2499-2506, 1992
 A/Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in
 A/Reference number: S30496; PMID:93096484; PMID:1281307
 A/Accession: S30497
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 611-667 <GIL>
 A/Cross-references: EMBL:X57236; NID:953187; PIDN:CAA40512.1; PID:953188
 C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prot
 C/Keywords: ATP; duplication; glycoprotein; growth factor receptor; phosphotransferase;
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/19-799/Product: fibroblast growth factor receptor 4 #status predicted <EXT>
 F/19-366/Domain: extracellular #status predicted <EXT>
 F/162-223/Domain: immunoglobulin homology <IMM>
 F/367-387/Domain: transmembrane #status predicted <TM>
 F/368-799/Domain: intracellular #status predicted <INT>
 F/462-747/Domain: protein kinase homology <KIN>
 F/470-478/Region: protein kinase ATP-binding motif
 F/54-98,169-221,268-330/Disulfide bonds: #status predicted
 F/500,517,609/Active site: Lys, Glu, Asp #status predicted

Query Match 5.7%; Score 123; DB 2; Length 799;
 Best Local Similarity 22.1%; Pred. No. 0.044;
 Matches 103; Conservative 45; Mismatches 136; Indels 182; Gaps 23;

QY 24 LGSSVALNCTAWVSGHCSLPSVQWLK----DGLPIGICGHSLHEYSWVKNLSEVLV 79
 DB 260 VGSDVELLCKVYSDAQPH-----IQMLKHVIVNGSSGADGFPYVQVLKTTDINISV-- 312

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OM protein - protein search, using sw model

Run on: August 1, 2005, 13:33:56 ; Search time 172 Seconds

(without alignments)
1220.654 Million cell updates/sec

Title: US-09-598-443-2

Perfect score: 2147
Sequence: 1 MGVCDRAAPFLSPSEDPVL.....GSRNYSARTDPTCLVSKDDM 410

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2147	100.0	410	2	09H733
2	2143	99.8	410	2	06IA17
3	1876	87.4	504	2	06UX13
4	1546.5	72.0	409	2	09JL28
5	267.5	12.5	686	1	IPL2_HUMAN
6	261	12.2	686	1	IPL2_MOUSE
7	257	12.0	695	1	IPL1_MOUSE
8	256.5	11.9	696	1	IPL1_HUMAN
9	256.5	11.9	696	1	IPL1_PANTR
10	256.5	11.9	696	1	IPL1_RAT
11	255.5	11.9	696	1	IPL1_PONPY
12	254	11.8	537	1	IRL8_MOUSE
13	240.5	11.2	570	1	ILAP_MACMU
14	231.5	10.8	541	1	IRI8_HUMAN
15	228.5	10.6	570	1	ILAP_HUMAN
16	224.5	10.5	539	2	08HX06
17	220	10.2	539	2	08AXT5
18	219	10.2	539	2	06YBY1
19	218.5	10.2	568	2	070YCS
20	217	10.1	574	1	IRL2_MOUSE
21	215.5	10.0	570	1	ILAP_MOUSE
22	213.5	9.9	569	2	06NMPS
23	211	9.8	533	2	09DEB1
24	210.5	9.8	533	2	ILAP_RAT
25	210	9.8	533	2	09DEB5
26	209.5	9.8	568	1	ILIR_HUMAN
27	207.5	9.7	560	2	06R175
28	206.5	9.6	561	1	IRL2_HUMAN
29	204.5	9.5	561	1	IRL2_RAT
30	204.5	9.5	569	2	06NMPS
31	203.5	9.5	573	2	09TV11

32	202	9.4	556	1	IRL1_HUMAN	001638 homo sapien
33	197	9.2	1058	2	076FY7	076fy7 tachpleus
34	196.5	9.2	1152	2	08MR5	08mr5 anopheles g
35	196.5	9.2	1152	2	07PC4	07pc4 anopheles g
36	196.5	9.2	1346	2	09V477	09v477 drosophila
37	191.5	8.9	573	2	08CBP3	08cbp3 mus musculus
38	190.5	8.9	573	2	08CBP3	08cbp3 mus musculus
39	190.5	8.9	576	1	ILIR_MOUSE	ilir304 mus musculus
40	189.5	8.8	567	1	IRL1_MOUSE	irl1 mus musculus
41	189	8.8	599	2	095256	095256 homo sapien
42	185	8.6	1356	2	08MR2	08mr2 anopheles g
43	184	8.6	555	2	090874	090874 gallus galli
44	183.5	8.5	571	2	08OFN4	08ofn4 salmo salar
45	183	8.5	566	1	IRL1_RAT	irl1 rat

ALIGNMENTS

RESULT 1
Q9H733 PRELIMINARY; PRT; 410 AA.
ID Q9H733
AC Q9H733
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DS Hypothetical protein FLJ21446 (SIGIRR protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isegai T., Sugano S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A.C., Sherechenko Y., Bouffard G.G.,
RA Whitting M., Madan A., Young A.C., Sherechenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RX Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK025099; BAB15066.1; -;
DR EMBL; BC025953; AAR25953.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR004075; ILL_receptor1.

DR InterPro: IPR000157; TIR.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO1537; INTRLNRI.F.
DR PROSITE: PSS0835; IG_LIKE; 1.
DR PROSITE: PSS0104; TIR; 1.
SQ SEQUENCE 410 AA; 45707 MW; 2A7A663D79567ED6 CRC64;

Query Match 100.0%; Score 2147; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2, 1e-173;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGVCDRADPFLSPSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVOMLKDGLPIGIG 60
DB 1 MPGVCDRADPFLSPSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVOMLKDGLPIGIG 60
QY 61 HYSLHEYSWVKANLSEVLVSIVGVNVTSTEVYGAFTCSIQNISFSFSLIQRAGPTSHVA 120
DB 61 HYSLHEYSWVKANLSEVLVSIVGVNVTSTEVYGAFTCSIQNISFSFSLIQRAGPTSHVA 120
QY 121 AVLASLLVLLALLALVYKCRNLVLLMYQDAYGVEVEINDGKYDAYVYSIDCPEDRKF 180
DB 121 AVLASLLVLLALLALVYKCRNLVLLMYQDAYGVEVEINDGKYDAYVYSIDCPEDRKF 180
QY 121 VNFILKPOLERRRGYKFLDDBDLPRAPPSADLVNLSRCRLIYVLSDAFLSRAMCSH 240
DB 121 VNFILKPOLERRRGYKFLDDBDLPRAPPSADLVNLSRCRLIYVLSDAFLSRAMCSH 240
QY 181 VNFILKPOLERRRGYKFLDDBDLPRAPPSADLVNLSRCRLIYVLSDAFLSRAMCSH 240
DB 181 VNFILKPOLERRRGYKFLDDBDLPRAPPSADLVNLSRCRLIYVLSDAFLSRAMCSH 240
QY 241 SFREGICRLLELTRRPIFFTFEGQRDPAPALRLRQHRHLVTLMLRPGSVTPSSDFW 300
DB 241 SFREGICRLLELTRRPIFFTFEGQRDPAPALRLRQHRHLVTLMLRPGSVTPSSDFW 300
QY 301 KEVQALPRKRYRYPVEGDPQTOLODDKPMILRGRVBEGRALDSEVPDPEGDIGVNG 360
DB 301 KEVQALPRKRYRYPVEGDPQTOLODDKPMILRGRVBEGRALDSEVPDPEGDIGVNG 360
QY 361 PVFGEPSAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410
DB 361 PVFGEPSAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410

RESULT 2
Q61A17 PRELIMINARY; PRT; 410 AA.
AC Q61A17;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SIGIRR protein.
GN Name=SIGIRR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schalten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: C9457338; CAG33619.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro: IPR001110; IG-1ike.
DR InterPro: IPR004075; IL1_receptor1.
DR InterPro: IPR000157; TIR.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO1537; INTRLNRI.F.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
DR PROSITE: PSS0104; TIR; 1.
SQ SEQUENCE 410 AA; 45689 MW; 2CBA663D79567ED6 CRC64;

Query Match 99.8%; Score 2143; DB 2; Length 410;
Best Local Similarity 99.8%; Pred. No. 4, 5e-173;
Matches 409; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGVCDRADPFLSPSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVOMLKDGLPIGIG 60
DB 1 MPGVCDRADPFLSPSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVOMLKDGLPIGIG 60
QY 61 HYSLHEYSWVKANLSEVLVSIVGVNVTSTEVYGAFTCSIQNISFSFSLIQRAGPTSHVA 120
DB 61 HYSLHEYSWVKANLSEVLVSIVGVNVTSTEVYGAFTCSIQNISFSFSLIQRAGPTSHVA 120
QY 121 AVLASLLVLLALLALVYKCRNLVLLMYQDAYGVEVEINDGKYDAYVYSIDCPEDRKF 180
DB 121 AVLASLLVLLALLALVYKCRNLVLLMYQDAYGVEVEINDGKYDAYVYSIDCPEDRKF 180
QY 121 VNFILKPOLERRRGYKFLDDBDLPRAPPSADLVNLSRCRLIYVLSDAFLSRAMCSH 240
DB 121 VNFILKPOLERRRGYKFLDDBDLPRAPPSADLVNLSRCRLIYVLSDAFLSRAMCSH 240
QY 241 SFREGICRLLELTRRPIFFTFEGQRDPAPALRLRQHRHLVTLMLRPGSVTPSSDFW 300
DB 241 SFREGICRLLELTRRPIFFTFEGQRDPAPALRLRQHRHLVTLMLRPGSVTPSSDFW 300
QY 301 KEVQALPRKRYRYPVEGDPQTOLODDKPMILRGRVBEGRALDSEVPDPEGDIGVNG 360
DB 301 KEVQALPRKRYRYPVEGDPQTOLODDKPMILRGRVBEGRALDSEVPDPEGDIGVNG 360
QY 361 PVFGEPSAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410
DB 361 PVFGEPSAPHTSGVSLGESRSSEVDVSDLSGRNYSARTDFYCLVSKDDM 410

RESULT 3
Q6UX13 PRELIMINARY; PRT; 504 AA.
AC Q6UX13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SIGIRR.
GN ORFName=UNQ301;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gunney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simone L., Singh J., Smith V., Stinson J., Vagtes A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie W.H., Yatsura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY358342; AAQ88708.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro: IPR001110; IG-1like.
DR InterPro: IPR004075; IL1_receptor1.
DR InterPro: IPR000157; TIR.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO1537; INTRLNRI.F.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
DR PROSITE: PSS0104; TIR; 1.
SQ SEQUENCE 504 AA; 55299 MW; B3D4A5A60AF19D28 CRC64;

Query Match 87.4%; Score 1876; DB 2; Length 504;

Best Local Similarity 96.8%; Pred. No. 2.6e-150;
Matches 360; Conservative 2; Mismatches 2; Indels 8; Gaps 1;

QY 1 MPQVCDAPPLPSSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVSQWMLKDGILGIGG 60
Db 1 MPQVCDAPPLPSSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVSQWMLKDGILGIGG 60
QY 61 HYSLHESWYKANSEVLSSVLGVNTSTEVYGAFTCSIONISFSSFTLORAGPTSHVA 120
Db 61 HYSLHESWYKANSEVLSSVLGVNTSTEVYGAFTCSIONISFSSFTLORAGPTSHVA 120
QY 121 AVIASLLVLLALLAALLLYKCRNLVLMYQDAYGEVEINDGKLYDAVYSYSDCPEDRK 180
Db 121 AVIASLLVLLALLAALLLYKCRNLVLMYQDAYGEVEINDGKLYDAVYSYSDCPEDRK 180
QY 181 VNFILKQLERRRRGYKFLDRLDRLPRAEPSADLLVLSRCRLIVLSDAFLSRACSH 240
Db 181 VNFILKQLERRRRGYKFLDRLDRLPRAEPSADLLVLSRCRLIVLSDAFLSRACSH 240
QY 241 SFRBGLCRLLELTRPIFTFEGQRDPAPALRLRHOHRLVTLMLRPGSVTPSSDFW 300
Db 241 SFRBGLCRLLELTRPIFTFEGQRDPAPALRLRHOHRLVTLMLRPGSVTPSSDFW 300
QY 301 KEVQALPRKVRYPVEGDPTQLQDDKDPMLILRGVPEGRALDSEVDPPEGDLGVRG 360
Db 301 KEVQALPRKVRYPVEGDPTQLQDDKDPMLILRGVPEGRALDSEVDPPEGDLGVRG 360
QY 361 PVFGSPAPPHPT 372
Db 359 -----PAOPHS 364

RESULT 4

Q9JLZ8 PRELIMINARY; PRT; 409 AA.
AC Q9JLZ8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE T011/interleukin-1 receptor 8.
GN Name=A1256711; Synonyms=TRR8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=14993616; DOI=10.1073/pnas.0308680101;
RA Garlinda C., Riva F., Polentarucci N., Buterchi C., Sironi M.,
RA De Bortoli M., Muzio M., Bergocini R., Scanziani E., Vecchi A.,
RA Hirsch E., Mantovani A.;
RT "Intestinal inflammation in mice deficient in Tlr8, an inhibitory
RT member of the IL-1 receptor family.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:3522-3526 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Benton-Rol G., Polentarucci N., Muzio M., Mantovani A.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113795; AAF26200.1;
DR MGD; MGI:134402; A1256711.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; I9.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR00157; TIR.
DR Pfam; PF00047; I9; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR SMART; SM00409; I9; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PSS0104; TIR; 1.
KM Receptor.
SO SEQUENCE 409 AA; 45707 MW; DC4AB99A72356A13 CRC64;

Query Match 72.0%; Score 1546.5; DB 2; Length 409;
Best Local Similarity 72.7%; Pred. No. 1.7e-122;
Matches 303; Conservative 32; Mismatches 67; Indels 15; Gaps 4;

QY 1 MPQVCDAPPLPSSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVSQWMLKDGILGIGG 60
Db 1 MAGCWDAPPLPSSEDOVLRLPALGSSVALNCTAMVSGPHCSLPVSQWMLKDGILGIGG 60
QY 61 HYSLHESWYKANSEVLSSVLGVNTSTEVYGAFTCSIONISFSSFTLORAGPTSHVA 120
Db 61 HFSLHEDFWANFSEI-VSSVVLNLTNEDYGTFCSYWNVSSHSFTLMRAGPAGHVA 119
QY 121 AVIASLLVLLALLAALLLYKCRNLVLMYQDAYGEVEINDGKLYDAVYSYSDCPEDRK 180
Db 120 AVIASLLVLLALLAALLLYKCRNLVLMYQDAYGEVEINDGKLYDAVYSYSDCPEDRK 179
QY 181 VNFILKQLERRRRGYKFLDRLDRLPRAEPSADLLVLSRCRLIVLSDAFLSRACSH 240
Db 180 VNFILKQLERRRRGYKFLDRLDRLPRAEPSADLLVLSRCRLIVLSDAFLSRACSH 239
QY 241 SFRBGLCRLLELTRPIFTFEGQRDPAPALRLRHOHRLVTLMLRPGSVTPSSDFW 293
Db 240 SFRBGLCRLLELTRPIFTFEGQRDPAPALRLRHOHRLVTLMLRPGSVTPSSDFW 292
QY 294 TPSSDFWKEVQALPRKVRYPVEGDPTQLQDDKDPMLILRGVPEGRALDSEVDPPEGDLGVRG 353
Db 293 TPSSDFWKEVQALPRKVRYPVEGDPTQLQDDKDPMLILRGVPEGRALDSEVDPPEGDLGVRG 352
QY 354 GDLGVRYPVEGRAPPHPTSGVSLGESRSSEVSDLSGSHYSAKTDYFCYVSKDM 410
Db 353 GDLGVRYPVEGRAPPHPTSGVSLGESRSSEVSDLSGSHYSAKTDYFCYVSKDM 409

RESULT 5

IPL2 HUMAN STANDARD; PRT; 686 AA.
ID IPL2 HUMAN
AC Q9NZP0; Q9NZP0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 05-JUN-2004 (Rel. 44, Last annotation update)
DE X-linked interleukin-1 receptor accessory protein-like 2 precursor
DE (IL1RAPL-2 related protein) (Interleukin-1 receptor 9) (IL-1R9) (IL-1
DE receptor accessory protein-like 2) (Three immunoglobulin domain-
DE containing IL-1 receptor-related 1) (TIGIR-1).
GN Name=IL1RAPL2; Synonyms=IL1R9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RA MEDLINE=20487553; PubMed=11031108; DOI=10.1006/geno.2000.6128;
RA Sana T.R., Debeys R., Timans J.C., Bazan J.F., Kastlein R.A.;
RT "Computational identification, cloning, and characterization of IL-
RT 1R9, a novel interleukin-1 receptor-like gene encoded over an
RT unusually large interval of human chromosome Xq22.2-q22.3.";
RL Genomics 69:252-262 (2000).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RA TISSUE=Liver;
RA MEDLINE=20459050; PubMed=10882729; DOI=10.1074/jbc.M004077200;
RA Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.;
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RA Grabowski M., Lorenz B., Hubel R., Strom T.M.;

RT "A gene (IL1RAPL-2) with 61% identity to IL1RAPL maps to Xq22.2.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RA MEDLINE=21472256; PubMed=11587848; DOI=10.1016/S0378-1119(01)00659-X;
RA Ferrante M.I., Ghilani M., Bulfone A., Franco B.;
RT "IL1RAPL2 maps to Xq22 and is specifically expressed in the central
RT nervous system.";
RL Gene 275:217-221(2001).
RN [5]
RP SEQUENCE OF 29-686 FROM N.A.
RX MEDLINE=20218565; PubMed=10757639; DOI=10.1038/sj.ejhg.5200415;
RA Jin H., Visevarajah R., Gardner R.J., Roberts R.G.;
RT "Two novel members of the interleukin-1 receptor gene family, one
RT deleted in Xp22.3-Xp21.3 mental retardation.";
RL Eur. J. Hum. Genet. 8:87-94(2000).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Detected at low levels in fetal and adult
CC brain, in particular in the frontal lobe, temporal lobe and
CC cerebellum. Detected at very low levels in skin, liver, fetal
CC ovary and placenta.
CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF212016; AAF61307.1; -;
DR EMBL; AF284436; AAG21370.1; -;
DR EMBL; AJ272208; CAB86868.1; -;
DR EMBL; AJ290436; CAB89867.1; -;
DR EMBL; AP181285; AAF59412.1; -;
DR HSSP; Q63345; 1PKO.
DR Genew; HGNC:5997; IL1RAPL2.
DR MIM; 300277; -;
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0004908; F:interleukin-1 receptor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR004077; IL1_receptor1p.
DR InterPro; IPR00157; TIR.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1539; INTRLEUKN1R2.
DR PRINTS; PRO1537; INTRLEUKN1R1F.
DR SMART; SM00409; IG; 3.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PSS0835; IG_LIKE; 3.
DR PROSITE; PSS0104; TIR; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 686 X-linked interleukin-1 receptor accessory
FT DOMAIN 17 354 Extracellular (Potential).
FT TRANSMEM 355 375 Transmembrane (Potential).
FT DOMAIN 376 686 Cytoplasmic (Potential).
FT DOMAIN 18 132 Ig-1like C2-type 1.
FT DOMAIN 141 232 Ig-1like C2-type 2.
FT DOMAIN 239 347 Ig-1like C2-type 3.
FT DOMAIN 400 559 TIR.
FT DISULFID 53 116 Potential.
FT DISULFID 162 214 Potential.
FT DISULFID 265 331 Potential.

FT CARBOHYD 63 63 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 211 211 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 328 328 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 686 AA, 78669 MW, E4007/BCD186957C CRC64;
Query Match 12.5%; Score 267.5; DB 1; Length 686;
Best Local Similarity 26.7%; Pred. No. 16-13;
Matches 111; Conservative 75; Mismatches 152; Indels 77; Gaps 21;
QY 6 DRAPDFLSPSEDQ--VLAPALGSSVALNCTAVV-VSGPHCSLPYQWLK-DGLPLGIGH 61
DB 237 DKPKKPLFEMENQPSVIDVQLKPINIPCKAFPGSGE--SGPMIYMKGEKFEELAGH 294
QY 62 YSLHEYSWKANLSE-----VLSSVLCVNVTSREYVAFPCSIONIS--FSSFTLOR 112
DB 295 IREGETRLKEHKEGEVELALIFPSVVRADLAN-----YTCHEENRGRKASVTLRK 348
QY 113 AGPTSHV--AAVLASLVLLALLLAALVVKCRNLVLMYODAYGEVEIN-DQKLYDAYV 169
DB 349 KDLIYKIELAGGLGALFLVLVLV--VIYKCYNIEMLFYRQHFAGDETNDNKEIDAYLV 406
QY 170 SYS-----DC--PEDRKFNFIKPOLERRRGYKFLDDRDLPRAPSDLVNLRS 220
DB 407 SYTKVQDQDTLDCDNPBEGFALEVLPDVLEKHYGYKFLPERDLIPSGTYMEDLTRVYG 466
QY 221 CRLIVYLS-DAFLSAWCSHSFREGCLRL--ELTRAPFITTEGGRRDPAHPRLRL 276
DB 467 SRRLIIVLPDPIYLRGWSIFELERLHMLVSGEI--KVILIECTELGKVCQVEBL 524
QY 277 ROHRHLVTLRLRPSGVTP--SSDFPKVEQLLPRVVRVRPVEGDPQDTQDDKDMLL 334
DB 525 KASIKLLSLIKWK-GSKSKLNSKFWKHLVYMPK-----KEML-- 564
QY 335 RGRVPEGRALDSEVPDPPEGDGVGPGVGPSPAPHTSGVSLGSRSEVPDVS 389
DB 565 -----PRCHVLDS-----AEQGLFGEIQLPISIMNTSRSATL--VSSQADLPE 605
RESULT 6
ID IPL2_MOUSE STANDARD; PRT; 686 AA.
AC Q9ER66; O9ER66;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE X-linked interleukin-1 receptor accessory protein-like 2 precursor
DE (IL1RAPL-2 related protein) (TIGIR-1).
GN Name=IL1RAPL2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Liver;
RX MEDLINE=20459050; PubMed=10882729; DOI=10.1074/jbc.M004077200;
RA Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=21472256; PubMed=11587848; DOI=10.1016/S0378-1119(01)00659-X;
RA Ferrante M.I., Ghilani M., Bulfone A., Franco B.;
RT "IL1RAPL2 maps to Xq22 and is specifically expressed in the central
RT nervous system.";
RL Gene 275:217-221(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.


```

FT SIGNAL 1 24 Potential.
FT CHAIN 25 695 X-linked interleukin-1 receptor accessory
FT DOMAIN 25 357 protein-like 1.
FT TRANSMEM 358 378 Extracellular (Potential).
FT DOMAIN 379 395 Cytoplasmic (Potential).
FT DOMAIN 25 134 Ig-like C2-type 1.
FT DOMAIN 143 232 Ig-like C2-type 2.
FT DOMAIN 242 350 Ig-like C2-type 3.
FT DOMAIN 403 561 TIR.
FT DISULFID 53 118 Potential.
FT DISULFID 164 216 Potential.
FT DISULFID 267 334 Potential.
FT CARBOHYD 63 63 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 122 122 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 138 138 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 213 213 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 264 264 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 331 331 N-linked (GLCNAC. . .) (Potential).
SQ SEQUENCE 695 AA; 79630 MW; 5FE34F204E5908B7 CRC64;

Query Match 12.0%; Score 257; DB 1; Length 695;
Best Local Similarity 26.2%; Pred. No. 8.2e-13;
Matches 95; Conservative 64; Mismatches 145; Indels 58; Gaps 17;

QY 6 DRAPDLSPSEDC--VLRPALGSSVALNCTAMVVSQPHCSLPVOMLKDGLPIGIGHYS 63
DB 239 DKPPKLLYPMESKLTVOETOLGGSSANLTCPAPFGYSGDVS-PLTYMK-----GEKF 289
QY 64 LHEYS---W-----VKANLSEVLVSVLVGVNTSTEVYGAFTCSIONIS---FSSFTL 110
DB 290 IEIDLERNVWESDIRLKEHLEGEQVSLIVDSVEGDLGNTSCVYENGNGRHASYLV 349
QY 111 QKAGPSTHVAVALSLVLLALLLALLYKC-RLNVLLMYQAYGEVEIN-DGKYDAY 168
DB 350 HKR-ELMYTVELAGGAILLLICSTVITYKCYKIEIMLYRNHFGAEIDGDNKDYDAY 408
QY 169 VVS-----DCEPRKFNPIILKPOLERRRGYLLPDDDLPRAPSAADLVNYS 219
DB 409 LSTYKDPDOMQOSTGEERFALILPDMLEKYGKFLPDDLLPTGN-----IEDVA 463
QY 220 RC---RLTIVLSDAF-LSRAWCSHFREGLCLLELT-RLPIFTFEGQRDPAPHAL 273
DB 464 RCDQSGRLIIVTPNVVARGMSIFELERLNNMLVTGSIKYLIECSLRGIMYQEV 523
QY 274 RLIRGRHVLTLILMR-EGSVTPSSDPKQVQALPRKAYRPV-----EGDPQTQ 323
DB 524 EALKHTIKLTLVIMKMGPKCNKLSKFKRLOQYEMPRK-RIEPIITHEQALDVSEQGFGE 582
QY 324 LQ 325
DB 583 LQ 584

RESULT 8
IPIL_HUMAN STANDARD; PRT; 696 AA.
ID IPIL_HUMAN STANDARD; PRT; 696 AA.
AC Q9NZN1; Q9U53;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE X-linked interleukin-1 receptor accessory protein-like 1 precursor
DE (IL1RAPL-1) (Oligophrenin-4) (Three immunoglobulin domain-containing
DE IL-1 receptor-related 2) (TIGIR-2).
GN Name=IL1RAPL; Synonyms=OPHN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., DISEASE, TISSUE SPECIFICITY, AND ALTERNATIVE
RP SPLICING.
RC TISSUE=Fetal brain;

```

```

RX MEDLINE=99400548; PubMed=10471494; DOI=10.1038/12623;
RA Carie A., Jun L., Benvenu T., Vinet M.-C., McConnell N., Couvert P.,
RA Zemi R., Cardona A., Van Buggenhout G., Frints S., Hamel B.,
RA Moraine C., Kopeck H.-H., Strom T., Howell G.R., Whitaker A.,
RA Ross M.T., Kahn A., Frys J.-P., Beldjord C., Marynen P., Chelly J.,
RA "A new member of the IL-1 receptor family highly expressed in
RA hippocampus and involved in X-linked mental retardation."
RA Nat. Genet. 23:25-31(1999).
RL [2]
RN SEQUENCE FROM N.A., AND DISEASE.
RX MEDLINE=20218565; PubMed=10757639; DOI=10.1038/sj.ejhg.5200415;
RA Jin H., Gardner R.J., Vismesvarajah R., Muntont F., Roberts R.G.,
RT "Two novel members of the interleukin-1 receptor gene family, one
RT deleted in Xp22.3-Xp21.3 mental retardation."
RL Eur. J. Hum. Genet. 8:87-94(2000).
RN [3]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=20459050; PubMed=10882729; DOI=10.1074/jbc.M004077200;
RA Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling."
RL J. Biol. Chem. 275:29946-29954(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/meg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.,
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees."
RL Mol. Biol. Evol. 20:1281-1289(2003).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.
CC -1- Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC -1- IsoId=Q9NZN1-1; Sequence=Displayed;
CC -1- TISSUE SPECIFICITY: Detected at low levels in heart, skeletal
CC muscle, ovary, skin, and in amygdala, caudate nucleus, corpus
CC callosum, hippocampus, substantia nigra and thalamus. Detected at
CC very low levels in tonsil, prostate, testis, small intestine,
CC placenta, colon and fetal liver.
CC -1- DISEASE: Defects in IL1RAPL are a cause of nonspecific X-linked
CC mental retardation (MRX34) [MIM:300426]. Several forms of X-linked
CC mental retardation have been described; they are classified as
CC non-specific if there are no other characteristic clinical
CC symptoms.
CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ243874; CAB56046.1; -
CC EMBL: AF181284; AAF59411.1; -
CC EMBL: AF284435; AAG21369.1; -
CC EMBL: AB102650; BAC81119.1; -
CC HSSP: F11362; 1EVT.
CC Genew: HGNC:5996; IL1RAPL.
CC MIM: 300426; -
CC GO: GO:0016020; C:membrane; ISS.
CC GO: GO:0004872; F:receptor activity; TAS.
CC GO: GO:0007611; P:learning and/or memory; TAS.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR004075; IL1_receptor1.

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Query Match	Similarity	Score	DB 1	Length
Beat local	26.5%	9.1e-13		696
Matches	95	Conservative	64	Mismatches 149; Indels 51; Gaps 15;
QY	6	DRAPDPLSPESDQ-VLRPALGVSSVALNCTAMVVGSPHCSLPYQWMLKDGRLGIGHYIS	63	
DB	239	DKRPPLVLPMSKLTIGTQLOGDSANLTCRAFGVSGVLS-PLIYMK-----GKXF	289	
QY	64	LHEYS---W-----VKANLSEVLVSSVLGVNTSTEVGAFTCISIONIS---FSSEFTL	110	
DB	290	IEDDENKVMESDIRILKEHLEGQGVSLIVDSVBEEDLNYSGVENGGRHNAVLL	349	
QY	111	QRAG--PFSVAVALASLLVLLALLAALLVYKCRNLVNLVYQDAYGEVEIN-DGKLYDA	167	
DB	350	HKRBLMYVLELAGGAILLLVLCVLT--IYKCYKIRBIMLEVRNHFGEELDGNKYDA	407	
QY	168	VVSYS-----DCEDRKRPVNILKPOLERRRGVYLPDDDDLPRAPPSADLVNLT	218	
DB	408	YLSTKVDPDQMNQSTGEERRPALEIRLDMLEKHNGVYLPFRDRLIPGTGVIDVAVCV	467	
QY	219	SRCRRLIVLSDAF-TSPACWSHSPREGICLYLELTR-RPIFITREGORPARPARLTL	276	
DB	468	DQSKRLIVMPPNVYVRGWSGIFLEETLRMLVGTGELKVLLECSSELRGLMAYQVEVAL	527	
QY	277	ROHRRLVTLILMR-PGSVTPSSDPEKVEQVALPRKVRVRYV-----EGDPQTOIQ	325	
DB	528	KHTIKLTLVIMKHGPKCNKLSKEFKRLQYEMPRK-RIEPTIHQALDVSEQGFGEIQ	585	
RESULT 9				
IP1	PANTR	STANDARD;	PRT;	696 AA.
AC	P60029;			
DT	29-MAR-2004 (Rel. 43, Created)			
DT	29-MAR-2004 (Rel. 43, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	X-linked interleukin-1 receptor accessory protein-like 1 precursor			
GN	(IL1RAPL-1) (Oligophrenin-4);			
OS	Name=IL1RAPL1; Synonyms=OPN4;			
OC	Pan troglodytes (Chimpanzee);			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.			
NCBI	TextID=9598;			
NN	[1]			

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RP SEQUENCE FROM N.A.
RA MEDLINE=22763540; PubMed=127753; DOI=10.1093/molbev/m9134;
RX Kifano T., Schwarz C., Nickel B., Pabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RL chimpanzees.";
RM Mol. Biol. Evol. 20:1281-1289(2003).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 TIR domain.
-----
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-----
DR EMBL; AB102651; BAC8120.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR00157; TIR.
DR Pfam; PF00047; IG_2.
DR Pfam; PF01582; TIR; 1.
DR PROSITE; PS50835; IG-LIKE; 3.
DR PROSITE; PS50104; TIR; 1.
DR GlycoProtex; Immunoglobulin domain; Receptor; Repeat; Signal;
KW Transmembrane.
PT SIGNAL 1 18 Potential.
PT CHAIN 19 696 X-linked interleukin-1 receptor accessory
PT FT protein-like 1.
PT FT DOMAIN 19 357 Extracellular (Potential).
PT FT TRANSMEM 358 378 Cytoplasmic (Potential).
PT FT DOMAIN 379 696 Intracellular (Potential).
PT FT DOMAIN 19 134 Ig-like C2-type 1.
PT FT DOMAIN 143 232 Ig-like C2-type 2.
PT FT DOMAIN 242 350 Ig-like C2-type 3.
PT FT DOMAIN 403 562 TIR.
PT FT DISULFID 53 118 Potential.
PT FT DISULFID 164 216 Potential.
PT FT DISULFID 267 334 Potential.
PT FT CARBOHYD 63 63 N-linked (GlcNAc...) (Potential).
PT FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
PT FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
PT FT CARBOHYD 213 213 N-linked (GlcNAc...) (Potential).
PT FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).
PT FT CARBOHYD 331 331 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 696 AA; 79968 MW; 9B7AD503D73CA9 CRC64;
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Query Match 11.9%; Score 256.5; DB 1; Length 696;
Best Local Similarity 26.5%; Pred. No. 9.1e-13;
Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15
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QY 6 DRAPDFLSPSDQ--VLRPALGSSVALNCTAMVVSQPHCSLPSYQWLKDGPLGIGHYS 63
DB DKPPLKLYPMESKLTIGETQGDASNLTCRAFFGVSGDVS-PLIYMK-----GKXF 289
QY 64 LHEYS-----W-----VKANISELVNVSIVGVNTSTREYGAFCISIONIS---FSSFTL 110
DB IEDDENRWMSDDRILIKHEHGEBOVSISLIVDSVEBGDLCNVCYENGNGRRHASYLL 349
QY 111 QRAG--PTSHAAVIALSLVLTALLLAALVVKGRNLVLYQOAYGVEVNI-DGKLYDA 167
DB 350 HKRELMTVVELAGLIGAILLVLCLVLT--IKYKXIEIMLFYRHHFGAEIJDGDKDYDA 407
QY 168 VVSYS-----DCEDEKRVNFILKPOLERRRGYKFLDRLDRLPRAEPSADLLVNL 218
DB 408 YLSYTKVDPDQMGNETGBEBSFALIEILPIMLEKGYKFLFIPDRDLIPGVYIDVARCV 467
QY 219 SRCRLIVLVSDAF-LSRAWCSHSFRRGLCRLELTR-RPIFTTFEGGRDPAPALRL 276
DB 468 DOSRRLIIVMTPNVYVVRGWSIFELERRLRMVLVTGEIKVILLICSESLRGIMNYQVEAL 527

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QY 277 RCRHRLVTLMLMR-PSGVTSPSSDFWKEVQALPRKYRYPV-----EGDPOTOLQ 325
 Db 528 KHTIKLITVTKMGPKCNKNSKFWKRLQYEMFPK-RIBPITHQALDVSEGGPFGLQ 585

RESULT 10
 ID IP1L RAT STANDARD; PRT; 696 AA.
 AC P59824;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE X-linked interleukin-1 receptor accessory protein-like 1 precursor (IL1RAPL-1).
 GN Name=Il1rapl1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Hippocampus;
 RA Boda B., Parisi L., Muller D.;
 RT "Full length cloning of rat IL1RAPL in the hippocampus."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 SIMILARITY: Belongs to the interleukin-1 receptor family.
 CC -1 SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1 SIMILARITY: Contains 1 TIR domain.
 CC -----
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 CC -----
 CC EMBL: AY16593; AAC62634.1; -
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR004075; IL1_receptor1.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00047; Ig; 2.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PRO1537; INTRKNI1RF.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS50104; TIR; 1.
 KM Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
 KM Transmembrane.
 FT CHAIN 1 24 Potential.
 FT 25 696 X-linked interleukin-1 receptor accessory
 FT DOMAIN 25 357 Extracellular (Potential).
 FT TRANSMEM 358 378 Extracellular (Potential).
 FT DOMAIN 379 696 Cytoplasmic (Potential).
 FT DOMAIN 25 134 Ig-like C2-type 1.
 FT DOMAIN 143 330 Ig-like C2-type 2.
 FT DOMAIN 242 350 Ig-like C2-type 3.
 FT DOMAIN 403 562 TIR.
 FT DISULFID 53 118 Potential.
 FT DISULFID 164 216 Potential.
 FT DISULFID 267 334 Potential.
 FT CARBOHYD 63 63 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 213 213 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 331 331 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 696 AA; 79771 MW; 3684FCCDD0AB3FD9 CRC64;

Query Match 11.9%; Score 256.5; DB 1; Length 696;
 Best Local Similarity 26.0%; Pred. No. 9, 1e-13;
 Matches 93; Conservative 64; Mismatches 152; Indels 49; Gaps 15;
 QY 6 DRAPDFLSPSEDO--VLRLPAGSSVALNCTANVWSPGHSLSVOMLKGGLPGIGGHS 63
 Db 239 DKRPKLYPMESKRLTQETOLGSAHLTRAFRGYSADV-PILYMK-----GEKF 289
 QY 64 LHEYS-----VKANLSEVLSSVLAGVNVSTEVYGAFTCSIONIS---FSSFTL 110
 Db 290 IEDLDENRWESDIRLKHLEQEVSLIYDSVEBGLGNYSCYVENGNRRHSLVLL 349
 QY 111 QRAGPTSHVAAYLASLVLALLLAALVYKC-RLNVLMLYODAYEVEIN-DGKYDAY 168
 Db 350 HKR-ELMYVELAGGALILLVCGVTVYKCYKIEIMLFYRNHFGAEELDGNKDYAD 408
 QY 169 VSY-----DCEDEKFPVNFILKPOLERRRGYKFLDDRDLPRAPPSADLVNYS 219
 Db 409 LSYTKVDPQMNQETGEERFALIELPMLKRYGKFLPRDLPTGTYTEVARCV 468
 QY 220 RCRRLIVLSDAF-LSRAWCSHSPREGLCRLLELTR-RPIFTFEGQRDPAPALRLR 277
 Db 469 QSRRLIVTPVYVVRKGSIFELTRLNMLVTGKIVLLCESELRGIMYQEVYALK 528
 QY 278 RCRHRLVTLMLMR-PSGVTSPSSDFWKEVQALPRKYRYPV-----EGDPOTOLQ 325
 Db 529 KHTIKLITVTKMGPKCNKNSKFWKRLQYEMFPK-RIBPITHQALDVSEGGPFGLQ 585

RESULT 11
 ID IP1L PONPY STANDARD; PRT; 696 AA.
 AC 07YOL9;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE X-linked interleukin-1 receptor accessory protein-like 1 precursor (IL1RAPL-1) (Oligophrenin-4).
 GN Name=IL1RAPL; Synonyms=OPHN4;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
 OC NCB1_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
 RA Kitano T., Schwarz C., Nickel B., Paabo S.;
 RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
 RT chimpanzees."
 RL Mol. Biol. Evol. 20:1281-1289(2003).
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 SIMILARITY: Belongs to the interleukin-1 receptor family.
 CC -1 SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1 SIMILARITY: Contains 1 TIR domain.
 CC -----
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 CC -----
 CC EMBL: AB102652; BAC81121.1; -
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00047; Ig; 2.
 DR Pfam: PF01582; TIR; 1.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS50104; TIR; 1.

KM Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
 FT SIGNAL 1 18 Potential.
 FT CHAIN 19 696 X-linked interleukin-1 receptor accessory protein-like 1.
 FT DOMAIN 19 357 Extracellular (Potential).
 FT TRANSMEM 358 378 Cytoplasmic (Potential).
 FT DOMAIN 379 696 Potential.
 FT DOMAIN 19 134 Ig-like 1.
 FT DOMAIN 143 232 Ig-like 2.
 FT DOMAIN 242 350 Ig-like 3.
 FT DOMAIN 403 562 TIR.
 FT DISULFID 53 118 Potential.
 FT DISULFID 164 216 Potential.
 FT DISULFID 267 334 Potential.
 FT CARBOHYD 63 63 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 122 122 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 138 138 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 213 213 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 264 264 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 331 331 N-linked (GlcNAc. . .) (Potential).
 FT SEQUENCE 696 AA; 79936 MW; 0332PEC31C2D4B1 CRC64;
 Query Match 11.9%; Score 255.5; DB 1; Length 696;
 Best Local Similarity 26.5%; Pred. No. 1.1e-12;
 Matches 95; Conservative 64; Mismatches 19; Indels 51; Gaps 15;
 QY 6 DRAPDLPSBDDQ-VLRPALGSSVALNCTAVVSGPHCSLPVQWLKDLPLGIGHS 63
 DB 239 DKPKLLPYESKLTIGETQGDANLTCRAFFGSGDVS-PLIYMK-----GEKF 289
 QY 64 LHEYS-----W-----VKALSEVLVSQVNTSTREYVGAFTCSIQNIS--FSSFTL 110
 DB 290 IEOLDENRVESDRIILKEHGEQVSIISLIVSVEGDIGVNSCYVENNGRRHSAVL 349
 QY 111 QRAG--PTSHVAAVLASLVLALLALALVVKRLNVLWYODAYGEVEIN-DGKLYDA 167
 DB 350 HKRELMTVYLAGLGLILLLVCLVT--IYCKKIKIMLPIYRHFABELDGNKYDA 407
 QY 168 YVYS-----DCPEDRKPFVNFILKPOLERRRGYKFLDDBLLPRAEPSADLLVNL 218
 DB 408 YLSYTKVDPMQMOGETGEERFALEILPDLMEKHYGKFLPDRDLPTGYIEDVAVCV 467
 QY 219 SRGRLLIVLSDAF-LSRACSHSFRGLCRLELT-RPIFTTPEQQRDPAPALRL 276
 DB 468 DQGRRLITVMTPTVYVARGMSIFELTRRLNMLVTGBIKYLIECSRLRGIIMYQVEAL 527
 QY 277 RQHRHLVTLTLMR-PGSVTPSPDPFKEVOLALPRKYVRV-----EGDPQQLQ 325
 DB 528 KHTIKLITVIMKMGPKCNKLNKFWKRLQYEMPEK-RIFPTTHEQALDVSEQGFELQ 585
 RESULT 12
 ID IR18 MOUSE STANDARD; PRT; 537 AA.
 AC 061058;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 receptor 1 precursor (IL1 receptor-related protein) (IL-1Rrp).
 GN Name=il18r1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. AND VARIANT ALA-317 DEL.
 RX MEDLINE=8623957; PubMed=8626725; DOI=10.1074/jbc.271.8.3967;
 RA Parrot P., Garik K.E., Bonner T.P., Dower S.K., Sims J.E.;
 RT "IL-1Rrp is a novel receptor-like molecule similar to the type I
 RT interleukin-1 receptor and its homologues TI/ST2 and IL-1R ACP.";
 RL J. Biol. Chem. 271.3967-3970(1996).

CC -1- FUNCTION: Receptor for interleukin 18 (IL-18). Binding to the
 CC agonist leads to the activation of NF-kappa-B.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- MISCELLANEOUS: Does not bind interleukin 1 alpha (IL-1A) or
 CC interleukin 1 beta (IL-1B).
 CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
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 CC -----
 DR EMBL: U43673; AAC52437.1; -.
 DR HSP: Q15399.1; PFV.
 DR MGD: MGI:105383; 118r1.
 DR InterPro: IPR003599; I9.
 DR InterPro: IPR007110; I9-like.
 DR InterPro: IPR004075; IL1_receptor1.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00047; I9_3.
 DR Pfam: PF01582; TIR_1.
 DR PRINTS: PRO1537; INTRKINRIF.
 DR SMART: SM00409; I9_2.
 DR SMART: SM00255; TIR_1.
 DR PROSITE: PSS0835; I9 LIKE, 1.
 DR PROSITE: PSS0104; TIR_1.
 KM Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Repeat;
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 537 Interleukin-18 receptor 1.
 FT DOMAIN 20 326 Extracellular (Potential).
 FT TRANSMEM 327 347 Potential.
 FT DOMAIN 348 537 Cytoplasmic (Potential).
 FT DOMAIN 33 102 Ig-like C2-type 1.
 FT DOMAIN 134 189 Ig-like C2-type 2.
 FT DOMAIN 212 312 Ig-like C2-type 3.
 FT DOMAIN 370 519 TIR.
 FT DISULFID 141 182 By similarity.
 FT DISULFID 234 296 By similarity.
 FT CARBOHYD 50 50 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 71 71 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 111 111 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 134 134 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 189 189 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 194 194 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 200 200 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 233 233 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 295 295 N-linked (GlcNAc. . .) (Potential).
 FT VARIANT 317 317 Missing.
 SQ SEQUENCE 537 AA; 61600 MW; B19FEA40335458 CRC64;
 Query Match 11.8%; Score 254; DB 1; Length 537;
 Best Local Similarity 27.9%; Pred. No. 1e-12;
 Matches 95; Conservative 64; Mismatches 113; Indels 70; Gaps 18;
 QY 9 PDLPSBDDQVLRPALGSSVALNCTA-----VVGSGPHCSLPVQ-----WLK 51
 DB 212 PALIGPKCEKV-GVEIGKVELNCSALNKDLPYMSIRKEDSDPVQCERKETTWS 270
 QY 52 DGLPLIGIGHYSLHEYSWYKANSEVLVSQVNTSTREYVGAFTCSION---ISPSF 108
 DB 271 EG-----KTHASKILTRPQ-----KITENYLVNLYNCTVANEADITKSF 309
 QY 109 TLQD---AGPTSHVAAVLASLVL--LALLAALLVVKRLNVLWYOD-AYGEVEINDG 162
 DB 310 VLVRKEIPDIPGHVPTFGVTVLVASVAVAVCIYLCVYKVDVLPFRRAABEDDTLTDG 369

RN [1]
 RP SEQUENCE FROM N.A. AND VARIANT ALA-317 DEL.
 RX MEDLINE=96222957; PubMed=8626725; DOI=10.1074/jbc.271.8.3967;
 RA Parnet P., Gerke K.E., Bonner T.P., Dower S.K., Sims J.E.;
 RT "IL-1R is a novel receptor-like molecule similar to the type I
 RT interleukin-1 receptor and its homologues T1/ST2 and IL-1R ACP";
 RL J. Biol. Chem. 271:3967-3970(1996).
 RP [2]
 RP SEQUENCE OF 19-29; 55-58; 59-71; 211-221; 222-231; 269-275; 276-280;
 RX 319-315 AND 524-535; AND CHARACTERIZATION.
 RX MEDLINE=97467370; PubMed=9325300; DOI=10.1074/jbc.272.41.25737;
 RA Torigoe K., Ushio S., Okura T., Kobayashi S., Tanai M., Kunikata T.,
 RA Murakami T., Sanou O., Kojima H., Fujii M., Ohta T., Ikeda M.,
 RA Ikegami H., Kurimoto M.;
 RT "Purification and characterization of the human interleukin-18
 RT receptor";
 RL J. Biol. Chem. 272:25737-25742(1997).
 CC -1- FUNCTION: Receptor for interleukin 18 (IL-18). Binding to the
 CC agonist leads to the activation of NF-kappa-B.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in lung, leukocytes, spleen, liver,
 CC thymus, prostate, small intestine, colon, placenta, and heart, and
 CC is absent from brain, skeletal muscle, pancreas, and kidney. High
 CC level of expression in Hodgkin's disease cell lines.
 CC -1- MISCELLANEOUS: Does not bind interleukin 1 alpha (IL-1a) or
 CC interleukin 1 beta (IL-1b).
 CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
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 CC -----
 DR EMBL, U43672; AAC50390.1; -.
 DR HSSP, Q15399; IPYV.
 DR Genew, HGNC:5988; IL18R1.
 DR MIM, 604494; -.
 DR GO, GO:0005886; C:plasma membrane; TAS.
 DR GO, GO:0004872; P:receptor activity; TAS.
 DR GO, GO:0006955; P:immune response; TAS.
 DR GO, GO:0007165; P:signal transduction; TAS.
 DR InterPro, IPR003599; Ig.
 DR InterPro, IPR007110; Ig-like.
 DR InterPro, IPR004075; IL1_receptor1.
 DR InterPro, IPR004074; IL1_receptor1/1.
 DR InterPro, IPR000157; TIR.
 DR Pfam, PF01582; TIR; 1.
 DR PRINTS, PRO1536; INTRLN1R12F.
 DR PRINTS, PRO1537; INTRLN1R1F.
 DR SMART, SM00409; IG_2.
 DR SMART, SM00255; TIR; 1.
 DR PROSITE, PSS0835; IG_LIKE; 1.
 DR PROSITE, PSS0104; TIR; 1.
 KM Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KM Polymorphism; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 18
 FT CHAIN 19 541 Interleukin-18 receptor 1.
 FT DOMAIN 22 329 Extracellular (Potential).
 FT TRANSMEM 330 350 Potential.
 FT DOMAIN 351 541 Cytoplasmic (Potential).
 FT DOMAIN 33 121 Ig-like C2-type 1.
 FT DOMAIN 133 121 Ig-like C2-type 2.
 FT DOMAIN 220 312 Ig-like C2-type 3.
 FT DOMAIN 373 523 TIR.
 FT DISULFID 140 185 By similarity.
 FT DISULFID 237 298 By similarity.
 FT CARBOHYD 91 91 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 150 150 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 197 197 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 236 236 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
 FT VARIANT 317 317 Missing.
 FT /FTID=VAR_014955.
 SQ SEQUENCE 541 AA; 62304 MW; 7173DB9C7EA71D32 CRC64;
 Query Match 10.8%; Score 231.5; DB 1; Length 541;
 Best Local Similarity 28.0%; Pred. No. 8.5e-11;
 Matches 99; Conservative 62; Mismatches 126; Indels 67; Gaps 19;
 QY 6 DRA---PDFLSPSDQVLRPALGSSVALNCTA-----WVSGPHCLSPYQWLKG 53
 DB 209 DRSNIVPLGLPKLNHV-AVELGKQVRLNCSALINEEDVYVMGEEGSDPNHIEKEM 267
 QY 54 LPLDIGHYSLHESWVKANSEYLVSSVAG---VNTSTVEYGAFTCSIGNISFSTTL 110
 DB 268 RIMTPEG-----KMHASKVLRLENIGESMLNV---LYNCTVASTGCTDKSFIL 313
 QY 111 QR---AGPTSHV--AAVLASLVLLALALALYKCRNLVLMYODAYGEVE-INDGX 163
 DB 314 VRKADMDIPGHVTRGMIITAVLVAVCVLYRVYDVLFLRHLTRDFTLTDGX 373
 QY 164 LYDAYVSY-SDC---PEDRKVFNIKPOLERRRGYKFLDDBDLPRAPSDALLVNL 218
 DB 374 TYDAFVSLKRECRNGBEHTFAVEILPRVLEKHFYKLCIFERDVVPGAVVDEIHLI 433
 QY 219 SRCRLRLVLSDALSL---RAMCSHFRGICR-----LLELRRLPIF-ITPEGQRDP 268
 DB 434 EKSRRLITVLSKSYNSNEVRELSGHELVKERIKIILIEFT--PTDFTFPQ---- 487
 QY 269 AHPALRLRGRHRLVTLWRPG-SYTPSSDFKREVOLAPRKRYRVPVEGDPQ 321
 DB 488 ---SLKLKSHR-----VLKMKADKSLSYNSRFWKNLILYMPAKI-VKRGDRDE 533
 RESULT 15
 ILAP HUMAN STANDARD; PRT; 570 AA.
 AC Q9NPH3; O14915; Q86WU7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-1 receptor accessory protein precursor (IL-1 receptor
 DE accessory protein) (IL-1RACP).
 GN Name=IL1RAP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND INTERACTION WITH IL1RI
 RP AND IL1RI.
 RC TISSUE=Placenta;
 RX MEDLINE=98058729; PubMed=9371760; DOI=10.1073/pnas.94.24.12829;
 RA Huang J., Gao X., Li S., Cao Z.;
 RT "Recruitment of IL1RI to the interleukin 1 receptor complex requires
 RT interleukin 1 receptor accessory protein";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12829-12832(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Saito T., Saito N.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INDUCTION BY
 RP PHORBOL ESTERS.
 RC TISSUE=Liver.
 RX MEDLINE=20261666; PubMed=10799889;
 RA Jensen L.E., Muzio M., Mantovani A., Whitehead A.S.;

RT "IL-1 signaling cascade in liver cells and the involvement of a
RT soluble form of the IL-1 receptor accessory protein." ;
RL J. Immunol. 164:5277-5286(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4), AND INDUCTION BY PHORBOL
RP ESTERS.
RC TISSUE=Liver;
RC MEDLINE=22664804; PubMed=12781872;
RA Jensen L.E., Whitehead A.S.;
RT "Expression of alternatively spliced interleukin-1 receptor accessory
RT protein mRNAs is differentially regulated during inflammation and
RT apoptosis." ;
RL Cell. Signal. 15:793-802(2003).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Skin
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stajich W., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tomihata S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullenbach S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sedergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalka U., Smilans D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 118-179 FROM N.A. (ISOFORM 1).
RC MEDLINE=98140136; PubMed=9479509; DOI=10.1006/geno.1997.5113;
RA Dale M., Hammond D.W., Cox A., Nicklin M.H.;
RT "The human gene encoding the interleukin-1 receptor accessory protein
RT (IL1RAP) maps to chromosome 3q28 by fluorescence in situ hybridization
RT and radiation hybrid mapping." ;
RL Genomics 47:325-326(1998).
RN [7]
RP INTERACTION WITH IRAK2.
RC MEDLINE=22546438; PubMed=12659850; DOI=10.1016/S0006-291X(03)00385-1;
RA Boch J.A., Yoshida Y., Koyama Y., Wara-Aswapati N., Peng H., Unlu S.,
RA Auron P.E.;
RT "Characterization of a cascade of protein interactions initiated at
RT the IL-1 receptor." ;
RL Biochem. Biophys. Res. Commun. 303:525-531(2003).
RN [8]
RP TISSUE SPECIFICITY.
RC MEDLINE=22419343; PubMed=12530978; DOI=10.1016/S1074-7613(02)00514-9;
RA Smith D.E., Hanna R., Friend D., Moore H., Chen H., Farese A.M.,
RA MacVittie T.J., Virca G.D., Sims J.E.;
RT "The soluble form of IL-1 receptor accessory protein enhances the
RT ability of soluble type II IL-1 receptor to inhibit IL-1 action." ;
RL Immunity 18:87-96(2003).
RN [9]
RP FUNCTION: Mediates interleukin-1-dependent activation of NF-kappa-
RP B. Isoform 1 is part of the membrane-bound form of the IL-1
RP receptor. Signaling involves formation of a ternary complex
RP containing IL1RI, TOLLIP, MYD88, and IRAK1 or IRAK2. Isoform 2
RP modulates the response to interleukin by associating with soluble
RP IL1RI and enhancing interleukin-binding to the decoy receptor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1). Isoform
CC 2, isoform 3 and isoform 4 are secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoforms=4;
CC Name=1; Synonyms=Membrane-bound IL-1RAcP, mIL-1RAcP;
CC IsoId=Q9NPB3-1; Sequence=Displayed;

CC Name=2; Synonyms=Soluble IL-1RAcP, sIL-1RAcP;
CC IsoId=Q9NPB3-2; Sequence=VSP_008050; VSP_008051;
CC Name=3; Synonyms=Soluble IL-1RAcP-beta, sIL-1RAcP-beta;
CC IsoId=Q9NPB3-3; Sequence=VSP_008052;
CC Name=4;
CC IsoId=Q9NPB3-4; Sequence=VSP_008053;
CC TISSUE SPECIFICITY: Detected in liver, skin, placenta, thymus and
CC lung.
CC -1- INDUCTION: Phorbol ester treatment causes down-regulation of
CC isoform 1 and induction of isoform 2.
CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
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CC -----
CC EMBL; AF029213; AAB84059.1; -;
CC EMBL; AB006537; BAA25421.1; -;
CC EMBL; AF167343; AAF71687.1; -;
CC EMBL; AF167340; AAF71688.1; -;
CC EMBL; AF167335; AAF71688.1; JOINED.
CC EMBL; AF167336; AAF71688.1; JOINED.
CC EMBL; AF167337; AAF71688.1; JOINED.
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CC EMBL; AF167339; AAF71688.1; JOINED.
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CC EMBL; AF167335; AAF71689.1; JOINED.
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CC EMBL; AF167337; AAF71689.1; JOINED.
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CC EMBL; AF167339; AAF71689.1; JOINED.
CC EMBL; AF167340; AAF71689.1; JOINED.
CC EMBL; AF167341; AAF71689.1; JOINED.
CC EMBL; AF538730; AAQ01755.1; -;
CC EMBL; AF538731; AAQ01756.1; -;
CC EMBL; AF538732; AAQ01757.1; -;
CC EMBL; AF538733; AAQ01758.1; -;
CC EMBL; AF538734; AAQ01759.1; -;
CC EMBL; AF487335; AAQ49451.1; -;
CC EMBL; BC053621; AAH5621.1; -;
CC EMBL; AF016261; AAC39609.1; -;
CC Genew; HGNC:5995; IL1RAP.
CC MIM; 602626; -;
CC InterPro; IPR003599; Ig.
CC InterPro; IPR007110; Ig-1like.
CC InterPro; IPR004075; IL1_receptor1.
CC InterPro; IPR004074; IL1_receptor1/IL1.
CC InterPro; IPR000157; TIR.
CC Pfam; PF00047; Ig_2.
CC Pfam; PF01582; TIR_1.
CC PRINTS; PRO1536; INTRLNRI12F.
CC PRINTS; PRO1537; INTRLNRI1F.
CC SMART; SM00409; Ig_3.
CC SMART; SM00255; TIR_1.
CC PROSITE; PS00835; IG_LIKE; 2.
CC PROSITE; PS0104; TIR_1.
CC KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;
CC Repeat; Signal; Transmembrane.
CC STGNL 1 20
CC CHAIN 21 570 Potential.
CC DOMAIN 21 367 Interleukin-1 receptor accessory protein.
CC TRANSMEM 368 388 Extracellular (Potential).
CC DOMAIN 389 570 Potential.
CC DOMAIN 21 128 Cytoplasmic (Potential).
CC DOMAIN 141 230 Ig-like C2-type 1.
CC DOMAIN 242 348 Ig-like C2-type 2.
CC DOMAIN 403 549 Ig-like C2-type 3.
CC TIR.

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FT DISULFID 47 114 Potential.
FT DISULFID 137 181 Potential.
FT DISULFID 160 212 Potential.
FT DISULFID 266 332 Potential.
FT CARBOHYD 57 57 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 111 111 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 118 118 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 196 196 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 209 209 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 299 299 N-linked (GlcNAc. . .) (Potential).
FT VARSPLIC 351 356 VPAPRY -> GNRGCG (in isoform 2).
FT VARSPLIC 357 570 /Frida=VSP_008050.
FT VARSPLIC 302 570 Missing (in isoform 2).
FT VARSPLIC /Frida=VSP_008051.
FT ISHRTDETRTQILSIKKVTSDELKRSYVCHARSAKEVA
FT KAAVKOKVPAPRYTVELACFGATVLLVILVYHYVYL
FT EMVLFPYRAHFGTDETLIDGKEDIYVSARNAEDEFVLLT
FT LRGVLENEFGYKLCIFDRDSLPGIYVDETLSFIQSRRL
FT VVLSPNVYLGCTQALLBKAGLENMASRGNINVLVQYKAY
FT KETVKELKRAKTVLIVIKMKGEKSKTPQGRFMQLQVAMP
FT VKSPRRSSDEQGLSYSLKNV -> ASSKIHSGTGLMFW

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Query Match 10.6%; Score 228.5; DB 1; Length 570;

Best Local Similarity 27.6%; Pred. No. 1.6e-10;

Matches 91; Conservative 60; Mismatches 150; Indels 29; Gaps 11;

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QY 9 PDFLSPESDQVLRPALGSSVALNCTAWVSGPHCSLPVQWLKDG-LPLGIGHYSLHEY 67
DB 243 PVJHSPNDHYVYKEPGEBILLIPCTVY-FGFIMDSRNEVWMTIDGKKDDITDVTINE- 300
QY 68 SWKANSSEVLVSSVLCV-NVTSTEVYGAFTC--STQNTSFSSFTLQRAQPTSHVAVL 123
DB 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAKEVAKAAVKOKVPAPRYTVEL 360
QY 124 A---SLVLALALLALLLVYKCRNLVLMYODAYGEVE-INDKLYDAYVSYSDCPEDRK 179
DB 361 ACGFGATVLLVILVYHYVYVW-LEMVLFYRAHFGTDETLIDGKEDIYVSARNAEDEFVLLT 419
QY 180 FVNFIILKPQLERRRGYKLFLLDRDLPRAPPSADLVNLSRCRLIYVLSDAFLSPRAMCS 239
DB 420 FVLLTLRGVLENEFGYKLCIFDRDSLPGIYVDETLSFIQSRRLVVLSPNVV----- 473
QY 240 HSPREGCLRLLELTRRPIFTFEG-----QRRDPAPALRLRQHRHLVTLILMR-PG 291
DB 474 ---LQGTQALLLELKAGLENMASRGNINVLVQYKAYKETVKELKRAKTVLIVIKMKGEK 530
QY 292 SVTPSSDFMKKVOLALPRKTVYRVEGDPQ 321
DB 531 SKYPOGRFMKQLOVAMPVKKSPRRSSDEQ 560

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